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Run on: October 6, 2004, 20:35:55 ; Search time 53 Seconds  
 (without alignments)  
 90.628 Million cell updates/sec

Title: US-09-982-259B-7  
 Perfect score: 89  
 Sequence: 1 GMTFRRAQEGAPLTGAACT  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282347505 residues  
 Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

maximum db seq length: 2000000000

Database 1

1: - genesedp1980s;\*  
2: genesedp1990s;\*  
3: genesedp2000s;\*  
4: genesedp2001s;\*  
5: genesedp2002s;\*  
6: genesedp2003as;\*  
7: genesedp2003bs;\*  
8: genesedp2004s;\*

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.

דוחות

result	Query				Description
	No.	Score	Match	Length	
				DB	ID
1	89	100.0	17	5	ABBT78091
2	72	80.9	14	6	ABU51976
3	72	80.9	14	6	ABU62398
4	72	80.9	322	2	AAV19985
5	72	80.9	339	2	AAW61757
6	72	80.9	339	2	AAV19984
7	69	77.5	340	2	ABR31013
8	44.5	50.0	604	4	ABG22311
9	43.5	48.9	4924	4	AAJ70968
10	43.5	48.9	4928	2	AAJ39300
11	43.5	48.9	4933	6	ABP57681
12	43	48.3	616	2	ABBB3900
13	42	47.2	341	2	ABR33280
14	42	47.2	341	2	AAW61758
15	41	46.1	130	5	ABG76529
16	41	46.1	247	3	AAY95746
17	41	46.1	247	7	ABU63665
18	41	46.1	1366	4	AAE10127
19	40	44.9	59	4	AAE01553
20	40	44.9	117	6	ADAS4805
21	40	44.9	196	5	ABP30378
22	40	44.9	200	5	ABP28344
23	40	44.9	328	6	AAE35494
24	40	44.9	339	4	AAY00049
25	40	44.9	339	5	ABDA2266

5	4.0	44.9	339	6	ABU88296
7	4.0	44.9	339	6	ABU13448
8	4.0	44.9	361	2	AAV03048
9	4.0	44.9	361	5	ABP43267
0	4.0	44.9	361	5	ABU88295
1	4.0	44.9	361	6	ABU13546
2	4.0	44.9	537	4	AAB96626
3	4.0	44.9	604	4	AAM42228
4	4.0	44.9	604	4	AABR57251
5	4.0	44.9	621	4	AAU33270
6	4.0	44.9	624	4	AAM42014
7	4.0	44.9	625	4	ABG2189
8	39.5	44.4	1891	2	AAW22610
9	39.5	44.4	1891	2	AAW23720
0	3.9	43.8	147	5	ABP11171
1	3.9	41.8	317	4	AAU41886
2	3.9	43.8	317	6	ABM8405
3	3.9	43.8	494	6	ABU33165
4	3.9	43.8	561	4	ABG04039
5	3.9	43.8	1168	5	ABP26042

RESULT 1	
ABB78091	ABB78091 standard; peptide; 17 AA.
XX	
AC	ABB78091;
XX	
DT	06-AUG-2003 (revised)
DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a <i>Borellia burgdorferi</i> epitope
XX	
KW	Epitope; polyethylene glycol; PEG; vaccine; Lyme disease

OS	Synthetic.	
OS	Borrelia burgdorferi.	
XX	Key	Location/Qualifiers
XX	Modified-site	15 /note= "beta alanine"
FT	FT	16 /note= "beta alanine"\n
FT	FT	WO200234117-A2.
XX	PN	02-MAY-2002.
XX	PD	22-OCT-2001; 2001WO-US046723.
XX	PF	24-OCT-2000; 2000US-0242819P.
PR	PR	17-OCT-2001; 2001US-00982264.
XX	PA	(UNN-1) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX	PI	Qiu B, Stein S, Zhang G, Sigal L, Brunner M, Katz M;
XX	DR	WPI; 2002-618962/66.
XX	PT	Ac immunological test kit for detecting analytes, comprising
XX	PT	composition of matter with an immunologically reactive sub-
PT	PT	Borrelia burgdorferi epitope polypeptide linked to an immu-
XX	PT	n invisible carrier.
XX	BS	Claim 51: Page 25; 36pp; English.
XX	CC	ABB78085-91 represent Borrelia burgdorferi epitope polypep-
CC	CC	ptides are conjugated in multiple copies to an immuno-
CC	CC	log invisible carrier. This carrier is preferably polyethylene
CC	CC	co-

Abu88295	E. faecal
Abu13547	Enterococ
Aay00048	Enterococ
Abp33267	E faecal
Abu88295	E. faecal
Abu13546	Enterococ
Aab96636	Putative
Aam40228	Human pol
Abr57251	Human mit
Aab53720	Novel hum
Aam42614	Human pol
Abg21889	Novel hum
Aaw22610	Platenoli
Aaw23120	Platenoli
Aau41171	Human ORF
Aau41886	Propionib
Abm32845	Propionib
Abu39165	Protein e
Abg04039	Novel hum
Abp26042	Streptoco

ALIGNMENTS	
RESULT 1	
ABB78091	ABB78091 standard; peptide: 17 AA.
ID	
XX	
AC	ABB78091;
XX	
DT	06-AUG-2003 (revised)
DT	05-NOV-2002 (first entry)
XX	Amino acid sequence of a <i>Borellia burgdorferi</i> epitope.
DE	
XX	
KW	Epitope; polyethylene glycol; PEG; vaccine; Lyme disease.

OS	Synthetic.	
OS	Borrelia burgdorferi.	
XX	Key	Location/Qualifiers
XX	Modified-site	15 /note= "beta alanine"
FT	FT	16 /note= "beta alanine"\n
FT	FT	WO200234117-A2.
XX	PN	02-MAY-2002.
XX	PD	22-OCT-2001; 2001WO-US046723.
XX	PF	24-OCT-2000; 2000US-0242819P.
PR	PR	17-OCT-2001; 2001US-00982264.
XX	PA	(UNN-1) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX	PI	Qiu B, Stein S, Zhang G, Sigal L, Brunner M, Katz M;
XX	DR	WPI; 2002-618962/66.
XX	PT	Ac immunological test kit for detecting analytes, comprising
XX	PT	composition of matter with an immunologically reactive sub-
XX	PT	Borrelia burgdorferi epitope polypeptide linked to an immu-
XX	PT	n invisible carrier.
XX	BS	Claim 51: Page 25; 36pp; English.
XX	CC	ABB78085-91 represent Borrelia burgdorferi epitope polypep-
CC	CC	ptides are conjugated in multiple copies to an immuno-
CC	CC	log invisible carrier. This carrier is preferably polyethylene
CC	CC	co-

CC peptides are used as vaccines, for immunising against or treating Lyme disease. They may also be used in an immunological test kit (such as enzyme linked immunosorbent assay (ELISA) kit, or immuno-capillary kit).  
 CC (Updated on: 06-AUG-2003 to correct OS field.)  
 XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 5; Length 17;  
 Best Local Similarity 100.0%; Prod. No. 5.2e-09;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GMTRFAQEGAAFTGAAAC 17  
 Db 1 GMTRFAQEGAAFTGAAAC 17

RESULT 2

ABU61976  
 ID ABU61976 standard; peptide; 14 AA.  
 XX

AC ABU61976;  
 XX  
 DT 25-AUG-2003 (First entry)  
 XX

DE Borrelia burgdorferii epitope p39.  
 XX  
 Epitope; vaccine; polyethylene glycol; PEG; ELISA; Lyme disease; enzyme linked immunosorbent assay; immuno-capillary kit.  
 XX

XX

FH Location/Qualifiers  
 FT Modified-site 14  
 PT /label= OTHER  
 FT /note= "GLY is linked to a (beta A) (beta A) C moiety  
 FT (not defined)."  
 XX

US200304127-A1.

XX

27-FEB-2003.

XX

17-OCT-2001; 2001US-0098265.

XX

24-OCT-2000; 2000US-0242819P.

XX

Qiu B.

Stein S.

Signal L.

Brunner M.

Katz M.

XX

PI Qiu B.

Stein S.

Signal L.

Brunner M.

Katz M.

XX

PI Qiu B.

Stein S.

Signal L.

Brunner M.

Katz M.

XX

PI Qiu B.

Stein S.

Signal L.

Brunner M.

Katz M.

XX

DR 2003-503407/47.

XX

PT Novel composition of matter for use in immunological test kit, comprises a first immunologically reactive substance connected to a second immunologically reactive substance by an immunologically invisible carrier.  
 XX  
 PS Disclosure; Page 5; 13pp; English.

RESULT 4

CC causative agent of Lyme disease  
 CC XX  
 CC Sequence 14 AA;  
 SQ

Query Match 80.9%; Score 72; DB 6; Length 14;  
 Best Local Similarity 100.0%; Prod. No. 5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GMTRFAQEGAAFTG 14  
 Db 1 GMTRFAQEGAAFTG 14

RESULT 3  
 ABU62398  
 ID ABU62398 standard; peptide; 14 AA.  
 XX

AC ABU62398;  
 XX  
 DT 01-SEP-2003 (first entry)  
 DE Lyme disease spirochete epitope polypeptide P39.  
 XX  
 DE Lyme disease spirochete; Lyme disease; immunological test kit; epitope; invisible carrier; P39.  
 XX  
 OS Borrelia burgdorferi.  
 XX  
 US200304126-A1.

PD 27-FBB-2003.  
 XX  
 PP 17-OCT-2001; 2001US-0098265.

XX

PP 24-OCT-2000; 2000US-0242819P.

XX

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CC causative agent of Lyme disease  
 CC XX  
 CC Sequence 14 AA;  
 SQ

Query Match 80.9%; Score 72; DB 6; Length 14;  
 Best Local Similarity 100.0%; Prod. No. 5e-06;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GMTRFAQEGAAFTG 17  
 Db 1 GMTRFAQEGAAFTG 17

RESULT 3

ABU62398

ID ABU62398 standard; peptide; 14 AA.

XX

AC ABU62398;

XX

DT 01-SEP-2003 (first entry)

XX

DB Lyme disease spirochete epitope polypeptide P39.

XX

KW Lyme disease spirochete; Lyme disease; immunological test kit; epitope;

XX

KW Lyme disease spirochete carrier; P39.

XX

OS Borrelia burgdorferi.

XX

PD 27-FBB-2003.

XX

PP 17-OCT-2001; 2001US-0098265.

XX

PR 24-OCT-2000; 2000US-0242819P.

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AAV19985  
 ID AAV19985 standard; protein; 322 AA.  
 XX  
 AC AAV19985;  
 XX  
 DT 19-JUL-1999 (first entry)  
 XX  
 DE B. burgdorferi antigenic protein, t541.aa.  
 XX  
 KW Antigenic protein; vaccine; Lyme disease; infection; detection.  
 OS Borrelia burgdorferi.  
 XX  
 PN W09859071-A1.  
 XX  
 PD 30-DEC-1998.  
 XX  
 PF 18-JUN-1998; 98WO-US012718.  
 XX  
 PR 20-JUN-1997; 97US-0050159P.  
 PR 22-JUL-1997; 97US-0053144P.  
 PR 22-JUL-1997; 97US-0053377P.  
 PR 03-SEP-1997; 97US-0057483P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (MEDI-) MEDIMMUNE INC.  
 PI Choi GH, Erwin AL, Hanson MS, Lathigra R;  
 XX  
 WPI: 1999-1B998C/16.  
 DR N-PSDB; AAX61682.  
 XX  
 PT New isolated Borrelia burgdorferi nucleic acids - used to develop  
 PT products for the diagnosis, prevention and treatment of diseases caused  
 PT by Borrelia, particularly Lyme disease.  
 XX  
 PS Claim 12; Page 150, 275PP; English.  
 XX  
 CC This sequence represents a Borrelia burgdorferi (Bb) protein of the  
 CC invention, which is suitable for use in a vaccine. The Bb polypeptides  
 CC can be used in vaccines for eliciting protective antibodies to members of  
 CC the Borrelia genus, particularly for the use against Lyme disease in  
 CC humans and animals. They can be used for preventing or attenuating an  
 CC infection caused by a member of the Borrelia genus. The products can also  
 CC be used for detection of members of the Borrelia genus.  
 XX  
 SQ Sequence 322 AA;  
 XX  
 Query Match 80.9%; Score 72; DB 2; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 0.00016;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PR 09-SEP-1998 (first entry)  
 XX  
 DE B. burgdorferi antigenic protein, f541.aa.  
 XX  
 KW Borrelia burgdorferi; antigenic protein p39 alpha.  
 KW Borrelia burgdorferi; Lyme disease.  
 XX  
 OS Borrelia burgdorferi.  
 XX  
 PN US5780041-A.

AAV19985  
 ID AAV19985 standard; protein; 322 AA.  
 XX  
 AC AAV19985;  
 XX  
 DT 01-MAR-1995; 95US-00396957.  
 XX  
 PR 05-MAR-1990; 90US-00487716.  
 PR 05-MAR-1991; 91US-00664731.  
 PR 19-FEB-1993; 93US-00020245.  
 XX  
 PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Schwan TG, Simpson WJ;  
 XX  
 WPI: 1998-41301/35.  
 DR N-PSDB; AAV19985; AAV35685.  
 XX  
 PT New antigenic proteins from Borrelia burgdorferi useful in vaccines - for  
 PT raising antibodies or for diagnostic detection of specific antibodies.  
 XX  
 PS Claim 1; Col 29-32; 33PP; English.  
 XX  
 CC This represents the Borrelia burgdorferi antigenic protein p39 alpha  
 CC which is immunoreactive with mammalian Lyme borreliosis serum. The  
 CC Borrelia antigenic proteins p39 alpha and p39 beta are used in vaccines  
 CC to protect against Lyme disease, as assay reagents to detect specific  
 CC antibodies in the serum (diagnostic of Lyme disease), and to raise  
 CC antibodies, either for diagnosis (by detecting the corresponding antigen)  
 CC or in screening agents for ability to inhibit expression of the proteins  
 XX  
 SQ Sequence 339 AA;  
 XX  
 Query Match 80.9%; Score 72; DB 2; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 0.00017;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PR 01-JUN-1998 (first entry)  
 XX  
 DE B. burgdorferi antigenic protein, p39 alpha.  
 XX  
 KW Antigenic protein; vaccine; Lyme disease; infection; detection.  
 XX  
 OS Borrelia burgdorferi.  
 XX  
 PN W09859071-A1.  
 XX  
 PD 30-DEC-1998.  
 XX  
 PR 18-JUN-1998; 98WO-US012718.  
 XX  
 PR 20-JUN-1997; 97US-0050354P.  
 PR 22-JUL-1997; 97US-0053344P.  
 PR 03-SEP-1997; 97US-0057483P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (MEDI-) MEDIMMUNE INC.  
 XX  
 PI Choi GH, Erwin AL, Hansson MS, Lathigra R;  
 XX  
 DR WPI: 1999-1B998C/16.  
 XX  
 DR N-PSDB; AAX61682.  
 XX

PT New isolated *Borrelia burgdorferi* nucleic acids - used to develop products for the diagnosis, prevention and treatment of diseases caused by *Borrelia*, particularly Lyme disease.  
 PT Claim 12; Page 143-150; 275pp; English.  
 XX This sequence represents a *Borrelia burgdorferi* (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the *Borrelia* genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the *Borrelia* genus. The products can also be used for detection of members of the *Borrelia* genus.

Sequence 339 AA;

Query Match 80.9%; Score 72; DB 2; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMTFRAQEGAFLTG 14  
 Db 1.29 GMTFRAQEGAFLTG 142

RESULT 7

AAR31013 ID AAR31013 standard; protein; 340 AA.  
 XX AC AAR31013;

XX DT 25-MAR-2003 (revised)  
 DT 17-DEC-2001 (revised)  
 DT 11-MAY-1993 (first entry)  
 XX DE P39-alpha.  
 XX KW Polymerase chain reaction; PCR; primer; open reading frame; ORF; P39;  
 KW antigen; 39-alpha; 39-beta; serum; human; Lyme patient; p39-beta;  
 KW p39-alpha; promoter; -10; -35; ribosomal binding site; RBS.  
 XX CS *Borrelia burgdorferi*.  
 XX PN USN7664731-N.  
 XX PD 01-DBC-1992.  
 XX PF 05-MAR-1991; 91US-00664731.  
 XX PR 05-MAR-1990; 90US-004887716.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICE  
 XX PI Simpson WJ, Schwan TG;  
 XX DR WPI: 1993-017799/02.  
 XX DR N-PSDB; AAQ34672.  
 PT New *Borrelia burgdorferi* protein and DNA isolates - used in detection of Lyme borreliosis infection and in prodn. of antibodies and vaccines.  
 XX Disclosure: Page 36-39; 69pp; English.  
 PS

CC The sequences given in AAR31013 and AAR33280 represent the *B. burgdorferi* genes P39-alpha and P39-beta. The DNA encoding these proteins was isolated by polymerase chain reaction (PCR), using the primer sequences given in AAQ34673-76. This DNA contained two open reading frames (ORFs). It was therefore concluded that the P39 antigen which has been previously described is not one protein but two, 39-alpha and 39-beta. The P39 signal appears to be enhanced when both genes are present. Gene 1 encodes a 339 amino acid protein with a calculated molecular weight of 36,926 kD. The protein encoded by this gene which is reactive with serum from human Lyme patients. The ORF of gene 2 has been designated p39-beta. This

PT products for the diagnosis, prevention and treatment of diseases caused by *Borrelia*, particularly Lyme disease.  
 XX This sequence represents a *Borrelia burgdorferi* (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members of the *Borrelia* genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the *Borrelia* genus. The products can also be used for detection of members of the *Borrelia* genus.  
 XX Sequence 340 AA;

Query Match 77.5%; Score 69; DB 2; Length 340;  
 Best Local Similarity 92.9%; Pred. No. 0.00061;  
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GMTFRAQEGAFLTG 14  
 Db 1.30 GMTFRAQEGAFLTG 143

RESULT 8

ABG22311 ID ABG22311 standard; protein; 604 AA.  
 XX AC ABG22311;

XX DT 18-FEB-2002 (first entry)  
 XX DE Novel human diagnostic protein #22202.  
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.  
 KW Homo sapiens.  
 XX OS Homo sapiens.  
 XX PN WO200175067-A2.  
 XX PD 11-OCT-2001.  
 XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.  
 XX PR 23-APR-2000; 2000US-00649167.  
 XX PA (HYSEQ-) HYSEQ INC.  
 PI Drmanac RT, Liu C, Tang YT;  
 XX WPI; 2001-639362/73.  
 DR N-PSDB; AAS86498.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders

involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG0010-ABG03077 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this Patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

Sequence 604 AA;

Query Match 50.0%; Score 44.5; DB 4; Length 604;  
Best Local Similarity 58.3%; Pred. No. 32;  
Matches 10; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Qy 2 MTFRQEG-AFPTGAAAC 17

Db 546 MXFKASBGPAPPGAMC 562

RESULT 9

AAB0968 ID AAB0968 standard: protein; 4924 AA.

XX

AC AAB0968

XX

AC

XX

DT

XX

DE

XX

RESULT 10

AAY39300 ID AAY39300 standard: protein; 4928 AA.

XX

AC AAY39300;

XX

AC

FT /label= AT7  
 FT /note= 'Acyl transferase domain: part of extender module  
 7"  
 FT 4344..4638  
 FT /label= KR7  
 FT /note= 'Beta-ketoreductase domain: part of extender  
 module 7"  
 FT 4725..4807  
 FT /label= ACP7  
 FT /note= 'Acyl carrier protein domain: part of extender  
 module 7"  
 XX WO99463887-A1.  
 XX  
 XX PD 16-SEP-1999.  
 XX PF 16-FEB-1999;  
 XX PR 09-MAR-1998; 9805-00036987.  
 XX (DOWC ) DOW AGROSCIENCES LLC.  
 XX PI Baltz RH, Broughton MC, Crawford KP,  
 XX PI Treadway PJ, Turner JR, Madduri K, Mario DJ,  
 XX DR N-PSDB; AAZ21501.  
 XX WPI; 1999-551414/46.  
 XX DR  
 PT New spinosyn biosynthetic genes from *Saccharopolyspora spinosa*, useful  
 PT for production of insecticidal spinosyn compounds.  
 XX  
 XX PS Claim 1; Page 113-129; 190pp; English.  
 XX  
 CC This is the amino acid sequence of the product of the *spnD* gene. The  
 CC protein is involved in spinosyn biosynthesis. The *SpnD* gene is one of 23  
 CC genes and open reading frames contained in an 80kb DNA sequence AAZ21501.  
 CC Spinosyns are insecticidal microldes which are useful for the control of  
 CC arachnids, nematodes and insects. Biosynthesis of spinosyns occurs via  
 CC stepwise condensation and modification of carboxylic acid precursors via  
 CC generating a linear polyketide which is modified further. The DNA  
 CC sequence contains a central region of approximately 55kb which has  
 CC homology to the DNA encoding the polyketide synthases (PKS) of known  
 CC macrolyde producers. The spinosyn PKS DNA region contains 5 ORFs with  
 CC stop codons at the end of acyl carrier protein (ACP) domains. Together  
 CC the PKS polypeptides (AY39297-Y39301) of which this sequence is one,  
 CC form a complex consisting of an initiator module, *spnA*, and several  
 CC extender modules *spnB*-*spnE*. Each extender module adds a specific acetyl  
 CC Co-A precursor to a growing polyketide chain, and modifies the beta-keto  
 CC group in a specific manner. A module in a PKS polypeptide consists of  
 CC several domains with specific functions. The initiator module has an acyl  
 CC transferase (AT) domain, and an acyl carrier protein (ACP) domain. The  
 CC extender modules have the same domains plus a beta-ketoreductase (KR)  
 CC domain and optionally a beta-ketoreductase domain, a dehydratase (DH)  
 CC domain, and an enoyl reductase (ER) domain. The last extender module  
 CC terminates with a thioester domain. The products of the genes present in  
 CC the upstream region of the PKS genes have been assigned names *spnF*-*spnS*  
 CC AAY39302-Y39315 and are responsible for different modifications in  
 CC spinosyn biosynthesis. There are also two ORFs ORFL1 and ORFL16 present  
 CC immediately upstream of *spnS*, producing polypeptides AAY39316-Y39317, and  
 CC two ORFs ORF1 and ORF2 present downstream of the PKS region producing  
 CC polypeptides AAY39318-Y39319. The genes are useful to improve yields of  
 CC spinosyns, and for creating new spinosyns e.g. by mutagenesis, or  
 CC interruption of steps in spinosyn biosynthesis. The modified spinosyns  
 CC may be a new insect control agent or serve as substrates for further  
 CC chemical modification and the creation of new semi-synthetic spinosyns.  
 CC The genes are also useful to isolate similar sequences from *S. spinosa* or  
 CC other species by hybridization  
 XX Sequence 4928 AA;  
 SQ Query Match 48.9%; Score 43.5; DB 2; Length 4928;  
 SQ Best Local Similarity 66.7%; Pred. No. 5et02;  
 SQ Marches 10; Conservative 2; Mismatch 2; Imbalance 1; Gaps 1;

Qy	1	GTTTAAQBGAAFLTG A	15
Db	3383	GTTT-VREGAAFLTG A	3396
<b>RESULT 11</b>			
	ABP57681		
ID	ABP57681	standard; protein; 4933 AA.	
XX			
AC	ABP57681;		
XX			
DT	22-JAN-2003	(first entry)	
XX			
DB	Saccharopolyspora busD	butenyl-spinosyn biosynthetic gene product.	
XX			
KW	Butenyl; biosynthetic enzyme; PKS; polyketide synthetase; macrolide; metabolite; spinosyn.		
XX			
OS	Saccharopolyspora sp.		
XX			
PN	WO200279477-A2.		
XX			
PD	10-OCT-2002.		
XX			
PF	28-MAR-2002; 2002WO-US009968.		
XX			
PR	30-MAR-2001; 2001US-0280175P.		
XX			
PA	(DOW ) DOW AGROSCIENCES LLC.		
XX			
PI	Hahn DR, Jackson JD, Bullard BS, Gustafson GD, Waldron C;		
PI	Mitchell JC;		
XX			
DR	WPI: 2003-058414/05.		
XX			
DR	NPDB; ABV75557.		
XX			
CC	The invention relates to a novel DNA molecule comprising a DNA sequence that encodes a butenyl-spinosyn biosynthetic enzyme, a butenyl-spinosyn PKS (polyketide synthetase) domain, or a spinosyn PKS module. The butenyl-spinosyn biosynthetic genes are useful for increasing the production of butenyl-spinosyn insecticidal macrolides, or for changing the metabolites or products produced by spinosyn-producing microorganisms.		
CC	Claim 1: Page 151-168; 218PP; English.		
CC	New butenyl-spinosyn biosynthetic genes, useful for increasing the production of butenyl-spinosyn insecticidal macrolides, or for changing the metabolites or products produced by spinosyn-producing microorganisms.		
XX	XX		
PS	Query Match Score 43.5; DB 6; Length 4933;		
XX	Best Local Similarity 66.7%; Pred. No. 5e+02;		
CC	Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps		
CC			
Qy	1	GTTTAAQBGAAFLTG A	15
Db	3380	GTTT-VREGAAFLTG A	3393
<b>RESULT 12</b>			
	ABB3900		
ID	ABB3900	Standard: dprotein; 616 AA	

Sequence 4928 AA;  
 Query Match 48.9%; Score 43.5; DB 2; Length 4928;  
 Best Local Similarity 66.7%; Prod. No. 5e02;  
 Marcher 10. Conservancy 2. Mammal 2. T-2020 1  
 AC ABB93900;  
 XX DT 31-MAY-2002 (first entry)

XX Herbicidal; plant; agriculture; herbicides.

XX WPI (USSH ) US DEPT HEALTH & HUMAN SERVICE.

XX Simpson WJ, Schwan TG;

XX DR WPI: 1993-017799/02.

XX DR N-PSDB; AAQ34672.

XX PT New *Borrelia burgdorferi* protein and DNA isolates - used in detection of Lyme borreliosis infection and in prodn. of antibodies and vaccines.

XX PT Disclosure; Page 36-39; 69pp; English.

XX CC The sequences given in AAR31013 and AAR33280 represent the *B. burgdorferi* proteins P39-alpha and P39-beta. The DNA encoding these proteins was isolated by Polymerase chain reaction (PCR) using the primer sequences given in AAQ34673-76. This DNA contained two open reading frames (ORF). It was therefore concluded that the P39 antigen which has been previously described is not one protein but two, 39-alpha and 39-beta. The P39 signal appears to be enhanced when both genes are present. Gene 1 encodes a 339 amino acid protein with a calculated molecular weight of 36,926 kD. The protein encoded by this gene which is reactive with serum from human Lyme patients. The ORF of gene 2 has been designated p39-beta. This gene's ORF starts 116 nucleotides downstream of p39-alpha and encodes a protein of 341 amino acids (37,506 kD). The promoter located 5' of p39-alpha appears to be present with classic -10 and -35 regions whereas p39-beta lacks a recognisable promoter sequence. Both genes have putative ribosomal binding sites immediately 5' to the start codons and each is terminated with a TAA codon. Comparing the gene sequences of p39-alpha and p39-beta indicates that these genes have 62% similarity. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at [www.derwent.com/drop1/updates/ntis\\_us.htm](http://www.derwent.com/drop1/updates/ntis_us.htm).) (Updated on 25-MAR-2003 to correct PPT field.)

SQ Sequence 341 AA;

Query Match 47.2%; Score 42; DB 2; Length 341;

Best Local Similarity 53.8%; Pred. No. 48;

Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 MTFRDAGAFLAG 14

Db 135 VYFVRDAGAFLAG 147

RESULT 14

AAW61758

ID AAW61758 standard; protein; 341 AA.

XX AC AAW61758;

XX DT 09-SEP-1998 (First entry)

DE B. burgdorferi antigenic protein p39 beta.

XX KW Borrelia burgdorferi; antigenic protein; p39 alpha; p39 beta; Lyme borreliosis; Lyme disease.

XX PD 14-JUL-1998.

XX PF 01-MAR-1995; 95US-00396957.

XX PR 05-MAR-1990; 90US-00487116.

XX PR 05-MAR-1991; 91US-00664731.

XX PR 19-FEB-1993; 93US-00020245.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

RESULT 13

AAR33280

ID AAR33280 standard; protein; 341 AA.

XX AC AAR33280;

XX DT 25-MAR-2003 (revised)

DT 17-DBC-2001 (revised)

DT 11-MAY-1993 (first entry)

XX DB P39-beta.

XX KW Polymerase chain reaction; PCR; primer; open reading frame; ORF; P39; antigen; 39-alpha; 39-beta; serum; human; Lyme patient; p39-beta; p39-alpha; promoter; -10; -35; ribosomal binding site; RBS.

XX OS *Borrelia burgdorferi*.

XX PN USN7664731-N.

XX PD 01-DBC-1992.

XX PF 05-MAR-1991; 91US-00664731.

XX PR 05-MAR-1990; 90US-00487116.

XX PR 19-FEB-1993; 93US-00020245.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

SQ Sequence 616 AA;

Query Match 48.3%; Score 43; DB 5; Length 616;

Best Local Similarity 57.1%; Pred. No. 61;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 TFRAGAFLAGTGA 16

Db 3: TPRSGENLYDGS 44

RESULT 13

AAR33280

ID AAR33280 standard; protein; 341 AA.

XX AC AAR33280;

XX DT 25-MAR-2003 (revised)

DT 17-DBC-2001 (revised)

DT 11-MAY-1993 (first entry)

XX DB P39-beta.

XX KW *Borrelia burgdorferi*.

XX OS *Borrelia burgdorferi*.

XX PN USN7664731-N.

XX PD 01-DBC-1992.

XX PF 05-MAR-1991; 91US-00664731.

XX PR 05-MAR-1990; 90US-00487116.

XX PR 19-FEB-1993; 93US-00020245.

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Schwan TG, Simpson WJ;  
 XX WPI: 1998-413001/35.  
 DR N-PSDE; AAV35685,  
 XX New antigenic proteins from *Borrelia burgdorferi* useful in vaccines - for  
 PT raising antibodies or for diagnostic detection of specific antibodies.  
 XX Example 6; Col 31-34; 33PP; English.  
 XX This represents the *Borrelia burgdorferi* antigenic protein p39 beta. The  
 CC antigenic protein p39 alpha is immunoreactive with mammalian Lyme  
 CC borreliosis serum. The *Borrelia* antigenic proteins p39 alpha and p39 beta  
 CC are used in vaccines to protect against Lyme disease, as assay reagents  
 CC to detect specific antibodies in the serum (diagnostic of Lyme disease),  
 CC and to raise antibodies, either for diagnosis (by detecting the  
 CC corresponding antigen) or in screening agents for ability to inhibit  
 CC expression of the proteins  
 XX Sequence 341 AA;  
 Query Match 47.2%; Score 42; DB 2; Length 341;  
 Best Local Similarity 53.8%; Pred. No. 48;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
 Qy 2 MTFFRAQEGFLTG 14  
 Db 135 VVERVEQQFLAG 147

RESULT 15  
 ABG76529  
 ID ABG76529 standard; Protein: 130 AA.  
 XX  
 AC ABG76529;  
 XX DT 05-NOV-2002 (first entry)  
 XX DB HCV E1 antigen monoclonal antibody #17.  
 XX Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;  
 KW hepatotropic; Fab; hypervariable region; E2 antigen; antibody.  
 XX Homo sapiens.  
 XX PN WO200261954-A1.  
 XX 08-AUG-2002.  
 XX PF 14-JAN-2002; 2002WO-SE000044.  
 XX PR 12-JAN-2001; 2001US-0260889P.  
 XX PA (KARO-) KAROLINSKA INNOVATIONS AB.  
 PI Drakenberg K, Persson MAA;  
 XX DR WPI: 2002-608502/65.  
 XX Vaccine comprising a human monoclonal antibody against hepatitis C virus  
 PT (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.  
 XX  
 PS Disclosure; Page 29-30; 64PP; English.  
 XX The invention relates to a human monoclonal antibody or its antigen  
 CC binding fragments, which exhibit immunological binding affinity for a  
 CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence  
 CC homologous to the binding portion of a human antibody Fab molecule from a  
 CC combinatorial antibody library. The vaccine composition comprising the  
 CC antibodies or antigen binding fragments useful in creating or preventing HCV  
 CC infection in a subject. Sequences ABG76513-ABG76568 represent human  
 CC monoclonal antibodies against HCV E1 antigen



C79009  
ABC transporter (lipoprotein) homolog yufN - *Bacillus subtilis*  
C:Species: *Bacillus subtilis*  
C:Accession: CT0009  
R:Kunst, F.; Ogawa, N.; Moszer, I.; Albertini, A.M.; Azevedo, V.; Berter, C.; Bron, S.; Bronville, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chai, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabbret, C.; Ferrari, E.; Nature 390, 249-256, 1997  
A;Authors: Faulkner, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galler, J.; Hilbert, H.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hull, M.P.; Koettner, P.; Konigstein, G.; Kirsch, S.; Kumano, M.; Kurita, K.; Lardinois, A.; Lardinois, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Masuda, S.; Mauel, Rieger, M.; Rivolta, C.; Roche, B.; Roche, B.; Rose, M.; Sadale, Y.; Saito, T.; Scanellier, A.; Schleicher, S.; Schroeter, R.; Scuffone, F.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Ueda, M.; Tamakoshi, A.; Tanaka, T.; terpstra, P.; Togimori, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yata, K.; Yoshida, A.; Authors: Yoshioka, H.; Zunstein, E.; Yoshihara, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.  
A;Reference number: A69580; PMID:9804033; MUID:3038377  
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-350 <UNK>  
A;Cross-references: GB:299120; GB:AL009126; NID:92635613; PIDN:CAA15143.1; PID:92635650  
C;Experimental source: strain 168  
C;Genetics:  
A;Gene: yufN  
C;Superfamily: ABC transporter yufN

Query Match 56.2%; Score 50; DB 1; Length: 350;  
Best Local Similarity 60.0%; Pred. No. 0.3%; 3; Mismatches 0; Gaps 0;  
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 MTFRQEGAFLTGAA 16  
Db 134 ITFKEQEGFLVGA 148

RESULT 3  
D64204  
membrane lipoprotein tmPC homolog - *Mycoplasma genitalium*  
C:Species: *Mycoplasma genitalium*  
C:Accession: D64204  
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; Merrick, J.; C.M.; Fuhrmann, J.-P.; Nguyen, D.; Utterback, T.R.; Sauder, D.M.; Phillips, C.A.; Merrick, J.; Science 270, 397-403, 1995  
A;Title: The minimal gene complement of *Mycoplasma genitalium*.  
A;Reference number: A64200; MUID:5626846; PMID:1563933  
A;Accession: D64204  
A;Status: Preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-591 <TIGR>  
A;Cross-references: GB:J39683; GB:L43967; NID:93844642; PIDN:AACT1256.1; PID:91045712; T  
A;Experimental source: strain G-37  
C;Genetics:  
A;Gene: yufN  
C;Superfamily: *Mycoplasma pneumoniae* probable lipoprotein D09\_orf657

Query Match 52.8%; Score 47; DB 2; Length 591;  
Best Local Similarity 53.3%; Pred. No. 1.8%; 3; Mismatches 3; Indels 0; Gaps 0;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 MTFRQEGAFLTGAA 16  
Db 180 VAFRSDQDSFLTGVVA 194

RESULT 4  
S73428  
probable membrane protein APE1877 - *Aeropyrum pernix* (strain Ki)  
C:Species: *Aeropyrum pernix*

C79009  
probable lipoprotein D09\_orf657 - *Mycoplasma pneumoniae* (strain ATCC 29342)  
N;Alternate names: MG040 homolog D09\_orf657  
C:Species: *Mycoplasma pneumoniae*  
A;Variety: ATCC 29342  
C;Date: 26-Feb-1997 #sequence\_revision 25-Apr-1997 #text\_change 15-Sep-2000  
R:Hummelreich, R.; Hilbert, H.; Plagens, H.; Pirkli, B.; Li, B.C.; Herrmann, R.; Nucleic Acids Res. 24, 4420-4449, 1996  
A;Title: Complete sequence analysis of the genome of the bacterium *Mycoplasma pneumoniae*  
A;Reference number: S73428  
A;Accession: S73428  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-657 <HIM>  
A;Cross-references: EMBL:AB00012; GS:U00089; NID:9167375; PIDN:AB95750.1; PID:916737  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996  
C;Genetics:  
A;Genetic code: SGCG3  
C;Superfamily: *Mycoplasma pneumoniae* probable lipoprotein D09\_orf657

Query Match 52.8%; Score 47; DB 2; Length 657;  
Best Local Similarity 53.3%; Pred. No. 2%; 3; Mismatches 3; Indels 0; Gaps 0;  
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
Qy 2 MTFRQEGAFLTGAA 16  
Db 176 VAFRSDQDSFLTGVVA 190

RESULT 5  
NDDB61  
exonuclease (EC 3.1.11.-) - *human herpesvirus 1* (strain 17)  
N;Alternate names: gene UL12 protein (deoxyribonuclease)  
C:Species: *human herpesvirus 1*  
A;Note: host Homo sapiens (man)  
C;Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 16-Jun-2000  
C;Accession: A00781; C30083  
R:McGeoch, D.J.; Dolan, A.; Frame, M.C.  
Nucleic Acids Res. 14, 3435-3448, 1986  
A;Title: DNA sequence of the region in the genome of herpes simplex virus type 1 containing the gene for the UL12 protein  
A;Reference number: A93620; MUID:86205244; PMID:3010237  
A;Accession: A00781  
A;Molecule type: DNA  
A;Residues: 1-226 <NCIG>  
A;Cross-references: GB:Y03839; NID:95981; PIDN:CAA27453.1; PID:59844  
R:McGeoch, D.J.; Dally, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perl, J.; Gen. Virol. 69, 1531-1574, 1988  
A;Title: The complete DNA sequence of the long unique region in the genome of herpes simplex virus type 1  
A;Reference number: A30083; MUID:88274327; PMID:2839594  
A;Title: DNA sequence of the region in the genome of herpes simplex virus type 1 containing the gene for the UL12 protein  
A;Molecule type: DNA  
A;Residues: 1-626 <NCIG>  
A;Cross-references: GB:X14112; NID:91944536; PIDN:CAA32325.1; PID:959513; GB:DC0317  
C;Genetics:  
A;Gene: UL12  
C;Superfamily: herpesvirus exonuclease  
C;Keywords: exonuclease; hydrolase

Query Match 50.6%; Score 45; DB 1; Length 626;  
Best Local Similarity 56.2%; Pred. No. 4.5%; 3; Mismatches 4; Indels 0; Gaps 0;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 MTFRQEGAFLTGAA 16  
Db 537 ITFKEQEGFLVGA 152

RESULT 6  
E72574  
probable membrane protein APE1877 - *Aeropyrum pernix* (strain Ki)  
C:Species: *Aeropyrum pernix*

C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 08-Sep-2000  
 C;Accession: E72574  
 C;Species: *Ureaplasma urealyticum*  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C;Accession: C82914  
 R;Glass, J.L.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 submitted to GenBank, February 2000  
 A;Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a minor  
 A;Reference number: A82870  
 A;Accession: C2914  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-525 <GLA>  
 A;Cross-references: GB:AB002123; GB:AF222694; NID:96899229; PIDN:AAFP30635.1; GSPDB:GNCC2  
 A;Experimental source: serovar 3; biovar 1  
 C;Genetics:  
 A;Gene: UU226  
 A;Genetic code: SGC3

## RESULT 7

C2214

conserved hypothetical membrane lipoprotein UU226 [imported] - *Ureaplasma urealyticum*  
 C;Species: *Ureaplasma urealyticum*  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C;Accession: C82914  
 R;Glass, J.L.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 submitted to GenBank, February 2000  
 A;Description: The complete sequence of *Ureaplasma urealyticum*: Alternate views of a minor  
 A;Reference number: A82870  
 A;Accession: C2914  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-525 <GLA>  
 A;Cross-references: GB:AB002123; GB:AF222694; NID:96899229; PIDN:AAFP30635.1; GSPDB:GNCC2  
 A;Experimental source: serovar 3; biovar 1  
 C;Genetics:  
 A;Gene: UU226  
 A;Genetic code: SGC3

Query Match 48.3%; Score 43; DB 2; Length 256;  
 Best Local Similarity 56.2%; Pred. No. 4.1;  
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 Qy 1 GMTFRAQEQAFLTGAA 16  
 Db 217 GIAFNAHVGGFLTGVA 232

## RESULT 9

B70147

basic membrane lipoprotein B (bmpB) - Lyme disease spirochete  
 C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)  
 C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 29-Sep-1999  
 C;Accession: E70147; 140242  
 R;Fraser, C.M.; Casten, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, D.; Peterson, J.; Kerlar, R.; Quackenbush, J.; Salzberg, S.; Hanlon, M.; Vugt, B.; Boeman, G.; Garibaldi, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Authors: Smith, H.O.; Venter, J.C.  
 A;Title: Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*.  
 A;Reference number: A70100; MUID:98065943; PMID:9403685  
 A;Accession: E70147  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-341 <KLE>  
 A;Cross-references: GB:AB001143; GB:AB00783; NID:92688279; PIDN: AAC66758.1; PID:92688;  
 A;Experimental source: strain B31  
 R;Simpson, W.J.; Cieplak, W.  
 PEMS Microbiol. Lett. 119, 381-388, 1994  
 A;Title: Nucleotide sequence and analysis of the gene in *Borrelia burgdorferi* encoding  
 A;Reference number: I40289; MUID:94327086; PMID:8050720  
 A;Accession: I40290  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-232; 'A', 234-317, 'V', 319-341 <RES>  
 A;Cross-references: GB:L24194; NID:9508420; PIDN:AAA72407.1; PMID:9508422  
 R;Chaimi, C.; Davidson, B.E.; Saint, Girons, I.; Old, I.G.  
 Microbiology 140, 2931-2940, 1994  
 A;Title: Conservation of gene arrangement and an unusual organization of rRNA genes in  
 A;Accession: I40242  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-44; 'A', 46-179 <RE2>  
 A;Cross-references: GB:L35050; NID:9516591; PIDN: AAC91402.1; PMID:9551744  
 C;Superfamily: basic membrane protein C

Query Match 48.3%; Score 43; DB 2; Length 525;  
 Best Local Similarity 53.3%; Pred. No. 8.7;  
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 2 MTFRAQEQAFLTGAA 16  
 Db 128 ITYRADQAFLGAGA 142

## RESULT 8

S45281

coagulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 10-Apr-1995 #sequence\_revision 22-Apr-1995 #text\_change 21-Jan-2000  
 C;Accession: S45281; A61329  
 R;Shibuya, Y.; Somba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.  
 Biochim. Biophys. Acta 1206, 63-70, 1994  
 A;Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): comp  
 A;Reference number: S45281; MUID:94242782; PMID:8186251  
 A;Accession: S45281  
 A;Molecule type: mRNA  
 A;Residues: 1-593 <SH1>  
 A;Cross-references: GB:S70164

A;Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 247 as Phe, CCG for residue 286 as G, is, and ATC for residue 505 as Leu  
 A;Cross-references: GB:S70164  
 A;Note: the authors translated the codon GAG for residue 23 as Val, GAG for residue 247 as Leu, CCG for residue 286 as G, is, and ATC for residue 505 as Leu  
 Qy 2 MTFRAQEQAFLTG 14  
 Db 135 VYFRVQGAFLAG 147

RESULT 10  
T40299  
Cystathione beta-synthase (EC 4.2.1.22) SPBC36.04 [similarity] - fission yeast (Schizosaccharomyces pombe)  
C;Species: Schizosaccharomyces pombe  
C;Accession: T40299 #sequence\_revision 03-Dec-1999 #text\_change 20-Jun-2000  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 20-Jun-2000  
C;Submitted to the EMBL Data Library, May 1998  
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Moestl, D.; Duesterh  
A;Reference number: Z21919  
A;Accession: T40299  
A;Status: preliminary; translated from GB/EMBL/DBSJ  
A;Gene: SPBC36.04  
A;Molecule type: DNA  
A;Map position: 2  
A;Introns: 45/1  
C;Superfamily: threonine dehydratase  
C;Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein; pyridoxal phosphate  
F;54/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted  
Query Match 47.2%; Score 42; DB 2; Length 351;  
Best Local Similarity 55.6%; Pred. No. 8.8;  
Matches 10; Conservative 2; Mismatches 4; Indels 2; Gaps 1;  
Qy 2 MTFRRA - QEGAGFLTGAC 17  
Db 274 MEFRLLDQEGFLPLGSSC 291  
  
RESULT 11  
F72418  
basic membrane protein - Thermotoga maritima (strain MSB8)  
C;Species: Thermotoga maritima  
C;Accession: F72418 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey  
C.M.; Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;  
Nature 399, 323-329, 1999  
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq  
A;Reference number: A72200; MJD:99287316; PMID:10360571  
A;Accession: F72418  
A;Status: preliminary  
A;Gene: TMSB8  
A;Molecule type: DNA  
A;Residues: 1-359 <ARN>  
A;Cross-references: GB:AB001696; GB:AE000512; NID:94980582; PIDN:AAD35196.1; PID:9498059  
A;Experimental source: strain MSB8  
C;Genetics:  
A;Gene: TMSB8  
C;Superfamily: ABC transporter yufN  
Query Match 47.2%; Score 42; DB 2; Length 359;  
Best Local Similarity 66.7%; Pred. No. 9;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
Qy 3 TERAQEGFLTG 14  
Db 122 TPKEQEGFLVG 133  
  
RESULT 12  
F72058  
AMP synthase - common tobacco (fragment)  
C;Contains: uridine monophosphate synthase  
C;Species: orotate phosphoribosyltransferase (EC 2.4.2.10); orotidine-5'-phosphate deca  
C;Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 18-Jun-1999  
A;Accession: T00508  
A;Submitted to the EMBL Data Library, March 1995  
C;Submitted to the EMBL Data Library, March 1995

A;Reference number: Z14527  
 A;Accession: T0058  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: mRNA  
 A;Residues: 1-161 <TH0>  
 A;Cross-references: EMBL:U22260; NIN:97477979; PIDN: AAC49115.1; PID:9747980  
 C;Experimental source: tissue-type leaf  
 C;Genetics:  
 A;Function:  
 A;Description: catalyzes conversion of orotidine 5'-phosphate and diphosphate to orotate and C02  
 A;Pathway: Pyrimidine metabolism  
 C;Superfamily: UMP synthase; orotate phosphoribosyltransferase homology; orotidine-5'-carbon-carbon lyase; carboxy-lyase; glycosyltransferase; pentosyltransferase  
 C;Keywords: carbon-carbon lyase; carboxy-lyase; pentosyltransferase; tissue-type leaf  
 Qy 3 TFRAGEGAFLTGAC 17  
 Qy 88 TAKALEGAFKPGQAC 102  
 Db  
 Db  
 RESULT 13  
 A84046  
 DNA Polymerase III alpha subunit dnab [imported] - *Bacillus halodurans* (strain C-125)  
 C;Species: *Bacillus halodurans*  
 C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 C;Accession: A8446  
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hi  
 Nucleic Acids Res. 28, 4311-4331, 2000  
 A;Title: Complete genome sequence of the aikaliphilic bacterium *Bacillus halodurans* and  
 A;Reference number: A83650; MUID:20512582; PMID:1105132  
 A;Accession: A8446  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-116 <STO>  
 A;Cross-references: GB:AP001517; GB:BA000004; NID:91017500; PIDN: BAB06388.1; GSPDB:GN  
 A;Experimental source: strain C-125  
 A;Gene: dnab  
 C;Superfamily: DNA-directed DNA polymerase III alpha chain  
 Qy 1 GMTFRQEGAFLTGAC 15  
 Qy 685 GEALRQBEAVTGAC 699  
 Db  
 Db  
 RESULT 14  
 B83007  
 conserved hypothetical protein PA5115 [imported] - *Pseudomonas aeruginosa* (strain PAO1)  
 C;Species: *Pseudomonas aeruginosa*  
 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C;Accession: B83007  
 R;Shover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; B  
 rdman, S.; Yuan, Y.; Brody, L.D.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim  
 Nature 406, 959-964, 2000  
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic path  
 A;Reference number: AB2950; MUID:20433737; PMID:10981043  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-194 <STO>  
 A;Cross-references: GB:AE004924; GB:AE004921; NID:99951407; PIDN: AAC008500.1; GSPDB:GN  
 C;Genetics:  
 A;Accession: B83007  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-194 <STO>  
 A;Cross-references: GB:AE004924; GB:AE004921; NID:99951407; PIDN: AAC008500.1; GSPDB:GN

A;Gene: PA5115

Query Match 46.1%; Score 41; DB 2; Length 194;  
 Best Local Similarity 80.0%; Pred. No. 7.2;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 EGAPLTGAAAC 17  
 Db 176 EGRFHTGAAAC 185

RESULT 15

CEBCEP  
cell division ATP-binding Protein ftsE - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 01-Mar-2002

C;Accession: S0131; S47682; B65143

R;Gill, D.R.; Hatfull, G.F.; Salmonod, G.P.C.

Mol. Gen. Genet. 205, 134-145, 1986

A;Title: A new cell division operon in Escherichia coli.

A;Reference number: S03129; MUID:3025556

A;Accession: S03131

A;Molecule type: DNA

A;Residues: 1-222 &lt;GIL&gt;

A;Cross-references: EMBL:X04398; NID:g41496; PIDN:CAA27985.1; PMID:g41499

R;Punkett, G.; submitted to the EMBL Data Library, March 1994

A;Reference number: S47682

A;Accession: S47682

A;Molecule type: DNA

A;Residues: 1-222 &lt;PLU&gt;

A;Cross-references: EMBL:U00039; NID:g466582; PIDN:AA818438.1; PMID:g466599

A;Rose, D.J.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64220; MUID:97426617; PMID:9278503

A;Accession: B65143

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-222 &lt;BLAT&gt;

A;Cross-references: GB:AB000422; GB:U00096; NID:91789868; PIDN:AA76488.1; PMID:g1789873;

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:  
A;Gene: ftsE

A;Map position: 76 min

C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology

C;Keywords: ATP; cell division; inner membrane; nucleotide binding; P-loop

F;18-213/Domain: ATP-binding cassette homology &lt;ABC&gt;

F;35-42/Region: nucleotide-binding motif A (P-loop)

F;158-163/Region: nucleotide-binding motif B

Query Match 46.1%; Score 41; DB 1; Length 222;  
 Best Local Similarity 62.5%; Pred. No. 8.3;  
 Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 GMTFRAGG-ATLTG 14  
 Db 20 GTTFFHMQGEMAFALTG 35

Search completed: October 6, 2004, 20:49:25  
 Job time : 18 secs

Scoring table:	BLOSUM62	Alignments	
Searched:	Gapop 10.0 , Gapext 0.5		
Total number of hits satisfying chosen parameters:	141681 seqs, 52070155 residues		
Minimum DB seq length:	0		
Maximum DB seq length:	200000000		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing First 45 summaries		
Database :	SwissProt_42:*		
	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
	SUMMARIES		
Result No.	Query Score	Match Length DB ID Description	
1	72	60.9 325 1 BMPA_BORGA	031557 borrelia ga
2	72	80.9 339 1 BMPA_BORAF	031280 borrelia af
3	72	80.9 339 1 BMPA_BORFU	045010 borrelia fu
4	50	56.2 350 1 YUFN_BACSU	005252 bacillus su
5	47	52.8 341 1 BMPB_BORAF	031184 borrelia af
6	47	52.8 341 1 BMPB_BORGA	031162 borrelia ga
7	47	52.8 591 1 Y040_MYCGE	P47286 mycoplasma
8	47	52.8 657 1 Y040_MYCP	P75062 mycoplasma
9	45	50.6 626 1 EXON_HSV1	P04244 herpes simp
10	43	48.3 593 1 PA12_BOVIN	P98140 bos taurus
11	42	47.2 448 1 Y4QG_RHISH	Q45011 borrelia bu
12	42	47.2 448 1 PYRS_TOBAC	P55628 rhizobium s
13	42	47.2 461 1 DP3A_BACHD	Q42942 nicotiana t
14	42	47.2 1116 1 FTSE_ECOL	Q9K638 bacillus ha
15	41	46.1 222 1 FTSE_ECOL	P10115 escherichia
16	41	46.1 410 1 AAB2_RHIME	P58950 rhizobium m
17	41	46.1 410 1 AAB2_RHIME	Q06191 rhizobium m
18	41	46.1 491 1 CPK3_ONCMY	093299 oncorthichu
19	41	46.1 504 1 CPK1_ONCMY	Q92090 oncorthichu
20	40	44.9 460 1 YWDJ_BACSU	P39518 bacillus su
21	40	44.9 492 1 GLPK_AQUAE	O66746 aquifex aeo
22	40	44.9 604 1 MAON_HUMAN	Q16798 human sapien
23	39	43.8 337 1 RIR2_TRYBBI	Q15210 trypansoma
24	39	43.8 338 1 RIR2_DICDI	P45211 dictyosteli
25	39	43.8 379 1 DN4J_PASHA	P05216 pasteurilla
26	39	43.8 646 1 LEFM_BOVIN	P42201 bos taurus
27	39	43.8 769 1 LEFM_SHEEP	P98109 ovis aries
28	38	43.3 629 1 GIDA_HAETIN	P44763 haemophilus
29	38	42.7 326 1 VS09_ROTEN	P04840 human rotavirus
30	38	42.7 341 1 BMPD_BORBU	Q47433 borrelia bu
31	38	42.7 345 1 RIR2_LELIAM	Q46310 leishmania
32	38	42.7 377 1 DN4J_HAEDU	P48208 haemophilus
33	38	42.7 420 1 SECf_TREPA	OB3426 treponema p

RESULT 1		
ID: BMPA_BORGA	STANDARD:	PRT: 325 AA.
AC: O31355;	AC: 031356;	
DT: 15-DEC-1998 (Rel. 37, Created)	DT: 15-DEC-1998 (Rel. 37, Last sequence update)	
DT: 10-OCT-2003 (Rel. 42, Last annotation update)	DB: Basic membrane protein A precursor (Fragment).	
DB: (Fragment).	GN: BMPA	
RA: Roessler D., Hauser U., Wilske B.	RA: Bacteriia; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia	
[1]	OS: Borrelia garinii	
RN: NCBI_TaxID=29519;	OX: NCBI_TaxID=29519;	
RP: Sequence from N.A.	RP: STRAIN=PBI, and PLI;	
RA: MBIDLINE=9801020;	RA: PubMed=9350727;	
RT: "Heterogeneity of BmpA (B39) among European isolates of Borrelia seroconversion lato and influence of interspecies variability on serodiagnosis.";	RT: burgdorferi sensu lato and influence of interspecies variability on serodiagnosis.;	
RL: Clin. Microbiol. 35:2752-2758 (1997).	CC: -!- FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN.	
	CC: -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (Probable).	
	CC: -!- SIMILARITY: Belongs to the BMP lipoprotein family.	
	CC: This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	
	CC: EMBL; X97244; CAA65883.1; -;	
	CC: EMBL; X97238; CAA65877.1; -;	
	DR: InterPro; IPR003760; Bmp.	
	DR: InterPro; IPR00437; Prok_lipoprot_S.	
	DR: Pfam; PP02608; Bmp; 1.	
	DR: InterPro; PS00013; PROKAR_LIPOPOTRIN; PARTIAL.	
	KW: Antigen; Membrane; Lipoprotein; Signal; Palmitate.	
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	FT: SIGNAL <1	
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	FT: LIPID 4	
	FT: LIPID 4	
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	FT: VARIANT 1400	
	FT: VARIANT 1405	
	FT: VARIANT 1410	
	FT: VARIANT 1415	
	FT: VARIANT 1420	
	FT: VARIANT 1425	
	FT: VARIANT 1430	
	FT: VARIANT 1435	
	FT: VARIANT 1440	
	FT: VARIANT 1445	
	FT: VARIANT 1450	
	FT: VARIANT 1455	
	FT: VARIANT 1460	
	FT: VARIANT 1465	
	FT: VARIANT 1470	
	FT: VARIANT 1475	
	FT: VARIANT 1480	
	FT: VARIANT 1485	
	FT: VARIANT 1490	
	FT: VARIANT 1495	
	FT: VARIANT 1500	
	FT: VARIANT 1505	
	FT: VARIANT 1510	
	FT: VARIANT 1515	
	FT: VARIANT 1520	
	FT: VARIANT 1525	
	FT: VARIANT 1530	
	FT: VARIANT 1535	
	FT: VARIANT 1540	
	FT: VARIANT 1545	
	FT: VARIANT 1550	
	FT: VARIANT 1555	
	FT: VARIANT 1560	
	FT: VARIANT 1565	
	FT: VARIANT 1570	
	FT: VARIANT 1575	
	FT: VARIANT 1580	
	FT: VARIANT 1585	
	FT: VARIANT 1590	
	FT: VARIANT 1595	
	FT: VARIANT 1600	
	FT: VARIANT 1605	
	FT: VARIANT 1610	
	FT: VARIANT 1615	
	FT: VARIANT 1620	
	FT: VARIANT 1625	
	FT: VARIANT 1630	
	FT: VARIANT 1635	
	FT: VARIANT 1640	
	FT: VARIANT 1645	
	FT: VARIANT 1650	
	FT: VARIANT 1655	
	FT: VARIANT 1660	
	FT: VARIANT 1665	
	FT: VARIANT 1670	
	FT: VARIANT 1675	
	FT: VARIANT 1680	
	FT: VARIANT 1685	
	FT: VARIANT 1690	
	FT: VARIANT 1695	
	FT: VARIANT 1700	
	FT: VARIANT 1705	
	FT: VARIANT 1710	
	FT: VARIANT 1715	
	FT: VARIANT 1720	
	FT: VARIANT 1725	
	FT: VARIANT 1730	
	FT: VARIANT 1735	
	FT: VARIANT 1740</td	

FT	VARIANT	257	N	-> S (IN STRAIN PLT).
SQ	SEQUENCE	325 AA;	35480 MW;	D19281A24B1C158 CRC64;
Query Match		80.9%;	Score 72;	DB 1; Length 325;
Best Local Similarity		100.0%;	Pred. No. 1.9e-05;	
Matches 14;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	GMTFRAQEAGAFLTG 14		
Db	115	GMTFRAQEAGAFLTG 128		
RESULT 2				
BMPA_BORAF				
ID	BMPA_BORAF	STANDARD;	PRT;	339 AA.
AC	Q31280; Q31281; Q31282; Q31283;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DB	Basic membrane protein A precursor (Immunodominant antigen P39).			
GN	BMPA			
OS	Borrelia afzelii			
OC	Bacteria; Spirochaetes; Spirochaetaceae; Borreliae.			
OX	NCBI_TaxID:29518;			
RN	NCBI_TaxID:29518;			
SEQUENCE FROM N.A. STRAIN=PKO, PWUD:, PLE, and PLJT;				
RC	MEDLINE=98010210; PubMed=9350727;			
RA	Roessler D.; Bauser U.; Wirsche B.;			
RA	"Heterogeneity of Bmpa (P39) among European isolates of Borrelia burgdorferi sensu lato and influence of interspecies variability on serodiagnosis."			
RT	J. Clin. Microbiol. 35:2752-2758(1997).			
RT	-!- FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN.			
CC	-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (Probable).			
CC	-!- SIMILARITY: Belongs to the BMP lipoprotein family.			
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EMBL	X84516; CAA5736.1; -.			
EMBL	X97237; CAA65826.1; -.			
EMBL	X97239; CAA65818.1; -.			
EMBL	X97241; CAA6580.1; -.			
InterPro	IPR0031760; Bmp.			
InterPro	IPR000437; Prok_lipoprot_S.			
Pfam	PF02608; Bmp; 1.			
PROSITE	PS00013; PROKAR_LIPOPROTEIN; FALSE NEG.			
Antigen	Membrane; Lipoprotein; Signal; Palmitate.			
Signal	1	17		
CHAIN	18	339		BASIC MEMBRANE PROTEIN A.
LIPID	18	18		N-palmitoyl cysteine (Probable).
LIPID	18	18		S-diacylglycerol cysteine (Probable).
VARIANT	125	125		
VARIANT	214	214		I -> T (IN STRAIN PLB).
VARIANT	229	229		A -> P (IN STRAIN PKO).
VARIANT	254	254		I -> V (IN STRAIN PLJT).
VARIANT	268	268		L -> F (IN STRAINS PLB AND PRO).
SEQUENCE	339 AA;	36966 MW;		1BEBADDF8CEA06FF4; CRC64;
Query Match		80.9%;	Score 72;	DB 1; Length 339;
Best Local Similarity		100.0%;	Pred. No. 2e-05;	
Matches 14;	Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;

RESULT	3
BMPA_BORBU	STANDARD ; PRT ; 339 AA.
ID	BORBU
AC	Q45010; P94249; Q44857;
DT	15-DEC-1998 (Rel. 37, Created)
DT	15-DEC-1998 (Rel. 37, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DB	Basic membrane protein A precursor (Immunodominant antigen 239).
GN	BMPA OR BB0363.
OS	<i>Borrelia burgdorferi</i> (lyme disease spirochete).
OX	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
NCBI TaxID	139;
RN	
RP	SEQUENCE FROM N.A.
RC	STRAIN=Sh-2; 82;
RX	Medline=94327086; PubMed=8050720;
RA	Thompson W.J., Cieplak W.R., Schrumpf M.E., Barbour A.G., Schwan T.G.,
RT	"Nucleotide sequence and analysis of the gene in <i>Borrelia burgdorferi</i> encoding the immunogenic P39 antigen." ;
RT	FEMS Microbiol. Lett. 119:381-388(1994).
RN	[2]
RN	SEQUENCE FROM N.A.
RC	STRAIN=297;
RX	Medline=97132632; PubMed=8978084;
RA	Aron L., Tobi C., Godfrey H.P., Cabello F.C.,
RT	"Identification and mapping of a chromosomal gene cluster of <i>Borrelia burgdorferi</i> containing genes expressed in vivo." ;
RT	FEMS Microbiol. Lett. 145:309-314(1996).
RN	[3]
RN	SEQUENCE FROM N.A.
RC	STRAIN=BL2016;
RA	Orlova T., Bugrysheva J., Novikova S., Godfrey H.P., Cabello F.C.,
RL	Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN	[4]
RN	SEQUENCE FROM N.A.
RP	STRAIN=ATCC 35210 / B31;
RX	Medline=98065943; PubMed=2403655;
RA	Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA	Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA	Dougherty B., Tomb J.-F., Richardson D., Richardson J.,
RA	Petersen J., Kerlavage A.R., Fleischmann R.D., Richardson S., Salzberg S., Hanson M.,
RA	van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.J.,
RA	Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA	Garfield S., Fujii C., Cotton M.D., Horst R., Roberts R., Hatch B.,
RA	Smith H.O., Venter J.C.,
RT	"Genomic sequence of a Lyme disease spirochete, <i>Borrelia burgdorferi</i> ." ;
RT	Nature 390:580-586 (1997).
RL	[5]
RN	SEQUENCE OF 248-339 FROM N.A.
RP	STRAIN=212;
RC	Medline=9511614; PubMed=7812434;
RX	Ojalvo C., Davidson B.E., Saint-Girons I., Old I.G.,
RT	"Conservation of gene arrangement and an unusual organization of rRNA genes in the linear chromosomes of the Lyme disease spirochaetes <i>Borrelia burgdorferi</i> , <i>B. garinii</i> and <i>B. afzelii</i> ." ;
RT	Microbiology 140:291-294(1994).
RBL	-1- FUNCTION: NOT KNOWN; IMMUNOGENIC PROTEIN.
CC	-1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (probable).
CC	-1- SIMILARITY: Belongs to the BMP lipoprotein family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation on the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
ENBL	I24194 AAA27406



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EMBL; X81519; CAA57239; 1; -  
InterPro; IPR003760; Bmp.  
Pfam; PF02608; Bmp; 1.  
PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
Membrane; Lipoprotein; Signal; Palmitole.  
STO: 1 14 PROBABLE.

FT CHAIN 15 341 BASIC MEMBRANE PROTEIN B.  
FT LIPID 15 15 N-palmitoyl cysteine (Probable).  
FT LIPID 15 15 S-diacylglycerol cysteine (Probable).  
SEQUENCE 341 AA; 37198 MW; 1E8EA3ID54ACDB1 CRC64;

Query Match 52.8%; Score 47; DB 1; Length 341;  
Best Local Similarity 57.1%; Pred. No. 0.65; Indels 0; Gaps 0;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GMTRFAQEGAFLTG 14  
Db 134 GYVFRIEQGAFLAG 147

RESULT 6  
BMPB\_BORG  
ID BMPB\_BORG  
STRAIN=P  
AC 031362;  
DT 15-DEC-1998 (Rel. 37, Created;  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DB Basic membrane protein B precursor.  
GN BMPB.  
OS Borrelia garinii.  
CC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
NCBI\_TAXID=29519;  
OX -  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=P; PMID=98010210; PubMed=93507227;  
RX MEDLINS=98010210; Pubmed=93507227;

RA Roessler D.; Hauser U.; Wilcke B.;  
RT "Heterogeneity of BmpA (P39) among European isolates of *Borrelia*  
burgdorferi sensu lato and influence of interspecies variability on  
serodiagnosis."  
RL J. Clin. Microbiol. 35:2752-2758 (1997).  
CC -!  
CC SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
(Probable).  
CC -! SIMILARITY: Belongs to the BMP Lipoprotein family.  
CC

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DR InterPro; IPR003760; Bmp.  
DR Pfam; PF02608; Bmp; 1.  
DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
KW Membrane; Lipoprotein; Signal; Palmitole.  
FT CHAIN 1 14 BASIC MEMBRANE PROTEIN B.  
FT LIPID 15 15 N-palmitoyl cysteine (Probable).  
FT LIPID 15 15 S-diacylglycerol cysteine (Probable).  
SEQUENCE 341 AA; 37236 MW; 442BBF05FEDDDC9A CRC64;

Query Match 52.8%; Score 47; DB 1; Length 341;  
Best Local Similarity 53.3%; Pred. No. 1.1; Indels 3; Mismatches 4; Gaps 0;

Query Match 52.8%; Score 47; DB 1; Length 341;  
Best Local Similarity 57.1%; Pred. No. 0.65; Indels 0; Gaps 0;  
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
Qy 1 GMTRFAQEGAFLTG 14  
Db 134 GYVFRIEQGAFLAG 147

RESULT 7  
Y040\_MYCCE  
ID Y040\_MYCCE  
AC P47286;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DR Hypothetical lipoprotein MG040 precursor.  
GN MG040.  
OS Mycoplasma genitalium.  
CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.  
NCBI\_TAXID=2197;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 33530 / G-37;  
RX MEDLINS=96026346; PubMed=7569993;  
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,  
Pleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,  
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,  
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,  
Tomb J.-P., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,  
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;  
RT "The minimal gene complement of Mycoplasma genitalium."  
RL Science 270:397-403 (1995).  
RN [2]  
RP SEQUENCE OF 448-517 FROM N.A.  
RC STRAIN=ATCC 33530 / G-37;  
RX MEDLINS=9075230; PubMed=8253680;  
RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III, Venter J.C.;  
RT "A survey of the Mycoplasma genitalium genome by using random  
sequencing."  
RL J. Bacteriol. 175:7918-7930 (1993).  
CC -! SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
(Potential).  
CC -! SIMILARITY: SOME TO T. PALLIDIUM TMPC.  
CC

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CC DR U39683; AAC71256; 1; -  
CC DR EMBL; U02125; AND12400; 1; -  
CC DR TIGR; MG040; -  
CC DR InterPro; IPR003760; Bmp.  
CC DR InterPro; IPR003437; Prok\_lipoprot\_S.  
CC DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
CC DR Hypothetical protein; Lipoprotein; Membrane; Signal;  
KW Complete proteome; Palmitole. POTENTIAL.  
FT SIGNAL 1 30  
FT CHAIN 31 591 HYPOTHETICAL LIPOPROTEIN MG040.  
FT LIPID 31 31 N-palmitoyl cysteine (Potential).  
FT LIPID 31 31 S-diacylglycerol Cysteine (Potential).  
SQ SEQUENCE 591 AA; 64019 MW;





STRAIN=ATCC 35210 / B31;	RESULT 12
RC MEDLINE=98010210; PubMed=9350727;	Y4QG_RHISN STANDARD; PRT; 448 AA.
RA Roessler D.; Hauser U.; Wilse B.;	ID Y4QG_RHISN
RT "Heterogeneity of BmpA (P39) among European isolates of <i>Borrelia burgdorferi</i> sensu lato and influence of interspecies variability on serodiagnosis.";	AC P55628;
RT [4]	DT 01-NOV-1997 (Rel. 35, Created)
RT RL	DT 01-NOV-1997 (Rel. 35, Last sequence update)
RN RP SEQUENCE FROM N.A.	DT 01-NOV-1997 (Rel. 35, Last annotation update)
RC STRAIN=ATCC 35210 / B31;	DE Probable aminotransferase Y4QG (EC 2.6.1.-).
RX MEDLINE=98065943; PubMed=9403685;	GN Y4QG.
RA Fraser C.M., Casjens H.W.M., Sutton G.G., Clayton R.A.,	RP SEQUENCE FROM N.A.
RA Lathigra R., White O., Ketchum K.A., Dodson R.K., Gwinn M.,	OS Rhizobium sp. (strain NGR234).
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,	OG Plasmid symbiont pNGR234a.
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,	OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
RA van Vugt R., Palmer N., Adams D.M., Gocayne J.D., Weidman J.,	OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
RA Utterback T., Wathey L., McDonald L., Artiach P., Bowman C.,	NCBI_TaxID=394;
RA Carlberg S., Fujii C., Cotton M.D., Horts K., Roberts K., Hatch B.,	RN
RA Smith H.O., Venter J.C.;	CC
RT "Genomic sequence of a Lyme disease spirochaete, <i>Borrelia burgdorferi</i> ";	CC
RL Nature 390:580-586(1997).	CC
RN	CC
RX SEQUENCE OF 1-179 FROM N.A.	CC
RC STRAIN=212;	CC
RX MEDLINE=95111614; PubMed=7812434;	CC
RA Ojaimi C., Davidson B.E., Saint-Girons I., Old I.G.,	CC
RA "Conservation of gene arrangement and an unusual organization of rRNA genes in the linear chromosomes of the Lyme disease spirochaetes <i>Borrelia burgdorferi</i> , <i>B. garinii</i> and <i>B. afzelii</i> .";	CC
RT Microbiology 140:12931-2940(1994).	CC
RT [-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor (Probable).]	CC
CC [-!- SIMILARITY: Belongs to the BMP lipoprotein family.	CC
CC	CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	CC
EMBL; L24194; AAA72407.1; -.	DR EMBL; AB000092; AAB91831.1; -.
EMBL; U49938; AAC44713.1; -.	DR HSSP; P12995; 1QJ3.
EMBL; X81517; CRA57237.1; -.	DR InterPro; IPR00814; Aminotrans_3.
EMBL; AE001143; AAC66758.1; -.	DR InterPro; IPR04637; Dat.
EMBL; L35050; AAC414021.1; -.	DR Pfam; PF00202; aminoran_3; 1.
PIR; B70147; B70147.	DR TIGR4MS; TIGR00709; dat_1.
DR InterPro; IPR00437.	DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PAUSE_NEG.
DR InterPro; IPR003760; Bmp.	KW Hypothetical protein; Aminotransferase; Transferase;
DR PROSITE; PS000013; PROKAP_LIPOPROTEIN_S.	KW Pyridoxal phosphate; Plasmid.
DR SIGNAL 1 14 PROBABLE.	FT BINDING 297 PYRIDOXAL PHOSPHATE (POTENTIAL).
DR KRW Membrane; Lipoprotein; Signal; Complete proteome; Palmitate.	SEQUENCE 448 AR; 49272 MW; 69982655PS3196CSA CRC64;
FT SIGNAL 1 14 PROBABLE.	Query Match 47.2%; Score 42; DB 1; Length 448;
FT CHAIN 15 341 BASIC MEMBRANE PROTEIN B.	Best Local Similarity 64.3%; Pred. No. 6.8; Mismatches 4; Indels 0; Gaps 0;
FT LIPID 15 15 N-Palmitoyl cysteine (Probable).	DB 326 TERGNNAFLVTGAA 339
FT LIPID 15 15 N-diacylglycerol cysteine (Probable).	CC
FT VARIANT 45 45 S (IN STRAIN B31).	RESULT 13
FT VARIANT 233 233 A > T (IN STRAIN B31).	PYR5_TOBAC STANDARD; PRT; 461 AA.
FT VARIANT 318 318 V > I (IN STRAIN B31).	ID PYR5_TOBAC
FT CONFLICT 53 53 R > P (IN REF. 3).	AC Q42922;
FT CONFLICT 67 67 S > P (IN REF. 3).	DT 01-NOV-1997 (Rel. 35, Created)
SQ SEQUENCE 341 AA; 37549 MW; C26AOD4BLDS2P39F CRC64;	DT 01-NOV-1997 (Rel. 35, Last sequence update)
Query Match 47.2%; Score 42; DB 1; Length 341;	DT 28-FEB-2003 (Rel. 41, Last annotation update)
Best Local Similarity 53.8%; Pred. No. 5.2; Mismatches 3; Indels 0; Gaps 0;	DE Uridine 5'-monophosphate synthase (OMP synthase) [Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRase); Orotate 5'-phosphate decarboxylase (EC 4.1.1.23) (OMPdecase)] (Fragment).
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	DB
CC	GN PYR5.
CC	OS Nicotiana tabacum (Common tobacco).
CC	OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC	OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; asterids;
CC	OC Lamiales; Solanales; Solanaceae; Nicotiana.
CC	NCBI_TaxID=4097;
CC	RN [1]

SEQUENCE FROM N.A.  
 RC STRAIN=cv. SRI; TISSUE=leaf;  
 RA Maier T.; Zhou L.; Thornburg R.W.;  
 RT "Nucleotide sequence of a cDNA encoding UMP synthase from Nicotiana tabacum."  
 RL (In) Plant Gene Register PGR95-025;  
 CC -|- CATALYTIC ACTIVITY: Orotidine 5'-phosphate + diphosphate = orotate + 5'-phospho-alpha-D-ribose 1-diphosphate.  
 CC -|- CATALYTIC ACTIVITY: Orotidine 5'-phosphate + CO(2) .  
 CC -|- PATHWAY: Pyrimidine biosynthesis; fifth and sixth (last) steps.  
 CC -|- SIMILARITY: In the N-terminal section; belongs to the purine/pyrimidine phosphoribotransferase family.  
 CC -|- SIMILARITY: In the C-terminal section; belongs to the decarboxylase family.  
 CC EMBL: U22260; AAC9115.1; - .  
 DR PIR: T02058; T02058.  
 DR HSSP: P03962; 1DQW.  
 DR InterPro: IPR01754; OMPdecase.  
 DR InterPro: IPR004467; Or phospho\_trans.  
 DR InterPro: IPR002375; Br7PY\_Dp\_Transf.  
 DR InterPro: IPR000836; PRtransfase.  
 DR Pfam: PF00215; OMPdecase; 1.  
 DR Pfam: PF00116; Ribosyltran; 1.  
 DR TIGRFAMS; TIGR00336; PyrE; 1.  
 DR PROSITE; PS00103; PUR PYR PR TRANSFER; 1.  
 DR PROSITE; PS00156; OMPDECASE; 1.  
 KW Pyrimidine biosynthesis; Multifunctional enzyme; Transferase;  
 KW Glycosyltransferase; Lyase; Decarboxylase.  
 FT NON\_TER 1  
 FT ACT\_SITE 291  
 SQ SEQUENCE 461 AA; 49760 MW; AA9647901957CD1 CRC64;  
 Query Match 47.2%; Score 42; DB 1; Length 451;  
 Best Local Similarity 60.0%; Pred. No. 7.1;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 Db 3 TFRAGQEGAGLTGAC 17  
 Db 88 TAKAIEGAKFKPSQAC 102

RESULT 14  
 DP3A\_BACHD STANDARD; PRT; 1116 AA.  
 AC DP3A\_BACHD (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE DNA Polymerase III alpha subunit (EC 2.7.7.7).  
 GN DNAE OR BH3169.  
 OS Bacteria; Firmicutes; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 NCBI\_TaxID:86665;  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C-125 / JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takami H.; Nakasone K.; Takaki Y.; Maeno G.; Sasaki R.; Masui N.;  
 RA Fuji F.; Hirama C.; Nakamura Y.; Ogasawara N.; Kihara S.;  
 RA Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and genomic sequence comparison with *Bacillus subtilis*."  
 RT Nucleic Acids Res. 28:4317-4331(2000).  
 RL -|- FUNCTION: DNA polymerase III is a complex, multichain enzyme

SEQUENCE FROM N.A.  
 CC This DNA polymerase also exhibits 3' to 5' exonuclease activity.  
 CC The alpha chain is the DNA polymerase (By similarity).  
 CC -|- CATALYTIC ACTIVITY: N deoxyribonucleoside triphosphate = N diphosphate + [DNA] (N).  
 CC -|- SUBUNIT: DNA polymerase III contains a core (composed of alpha, epsilon and theta chains) that associates with a *bau* subunit. This core dimerizes to form the POLIII complex. POLIII associates with the gamma complex (composed of gamma, delta, delta', psi and chi chains) and with the beta chain to form the complete DNA polymerase III complex (By similarity).  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -|- SIMILARITY: Belongs to the DNA polymerase type-C family. DnaE subfamily.  
 CC EMBL: AP001517; BAB06888.1; - .  
 DR PIR; AB4046; AB4046.  
 DR InterPro: IPR008994; Nucleic\_acid\_OB.  
 DR InterPro: IPR003141; PHP\_N.  
 DR InterPro: IPR004805; PolC\_alpha.  
 DR InterPro: IPR004165; tRNA\_anti.  
 DR Pfam: PF02231; PHP\_N; 1.  
 DR Pfam: PF01336; tRNA\_anti; 1.  
 DR SMART; SM00481; POLIITAC; 1.  
 DR TIGRFAMS; TIGR000994; PolC; 1.  
 KW Transferase; DNA-directed DNA polymerase; DNA replication;  
 KW Complete proteome.  
 SQ 1116 AA; 127531 MW; 97181EE0BFFD15F1 CRC64;

Query Match 47.2%; Score 42; DB 1; Length 1116;  
 Best Local Similarity 60.0%; Pred. No. 17;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

SEQUENCE FROM N.A.  
 ID FTSE\_ECOLI STANDARD; PRT; 222 AA.  
 AC P10115;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Cell division ATP-banding protein ftse.  
 GN FTSE OR B3463 OR C4256 OR Z4837 OR ECS4312 OR SF3481 OR S4282.  
 OS Escherichia coli;  
 OS Escherichia coli O157:H7; and  
 OS Shigella flexneri;  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 NCBI\_TaxID:562; 217392; 63334; 623;  
 RN [1] Sequence FROM N.A.  
 RP SPECIES=E.coli; STRAIN=K12;  
 RC MEDLINE=870903; PubMed=3025556;  
 RX Gill D.R.; Hattull G.F.; Salmon G.P.C.;  
 RA RT "A new cell division operon in *Escherichia coli*.";  
 RL Mol. Gen. Genet. 205:134-145 (1986).  
 RN [2] Sequence FROM N.A.  
 RP SPECIES=B.coli; STRAIN=K12 / MG1655;  
 RC MEDLINE=9431650; PubMed=8041620;  
 RX

RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R., "Analysis of the *Escherichia coli* genome. V. DNA sequence of the region from 76.0 to 81.5 minutes"; Nucleic Acids Res. 22:2576-2586(1994). [3]

RP SEQUENCE FROM N.A. SPECIES=*E. coli*; STRAIN=06:HL / CFT073 / ATCC 700928; MEDLINE=22388234; PubMed=12471157;

RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rosoch P., Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett J., Strand D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobile H.L.T., Donnenberg M.S., Blattner F.R.;

RA "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic *Escherichia coli*"; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

RN [4]

RP SEQUENCE FROM N.A. SPECIES=*E. coli*; STRAIN=0157:H7 / EDL933 / ATCC 700927;

RC MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Shao Y., Miller L., Postal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta B.T., Potanousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

RA "Genome sequence of enterohemorrhagic *Escherichia coli* 0157:H7"; Nature 409:529-533 (2001).

RN [5]

RP SEQUENCE FROM N.A. SPECIES=*E. coli*; STRAIN=0157:H7 / RIMD 0509952;

RC MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurikawa K., Ishii K., Yokoyama K., RA Iida T., Nakayama K., Murata T., Tobe T., Iida T., Takami H., Honda T., Sasakiwa C., Ogasawara N., Yasunaga T., RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RA "Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic comparison with a laboratory strain K-12.>"; DNA Res. 8:11-22 (2001).

RN [6]

RP SEQUENCE FROM N.A. SPECIES=*S. flexneri*; STRAIN=301 / Serotype 2a;

RC MEDLINE=22272406; PubMed=12384590;

RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong C., Sun L., Xie Y., Zhao A., Sun J., Zhu J., Gao B., Chen R., Ma D., Ding K., Chen S., Cheung H., Yao Z., He B., Chen R., Qiang B., Wen Y., Hou Y., Yu J.;

RA "Genome sequence of *Shigella flexneri* 2a: insights into pathogenicity through comparison with genomes of *Escherichia coli* K12 and O157.>"; DNA Res. 8:11-22 (2001).

RN [7]

RP SEQUENCE FROM N.A. SPECIES=*S. flexneri*; STRAIN=2457T / ATCC 700930 / Serotype 2a;

RC MEDLINE=22590274; PubMed=12704152;

RA Wei J., Goldberg M.B., Burland V., Verikasian M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., RA Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.;

RA "Complete genome sequence and comparative genomics of *Shigella flexneri* serotype 2a strain 2457T";

RT *Infect. Immun.* 71:2775-2786 (2003).

RL "-!- FUNCTION: NOT KNOWN. IS CODED IN AN OPERON ESSENTIAL FOR CELL DIVISION.

CC "-!- SIMILARITY: Belongs to the ABC transporter family.

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OM protein - protein search, using sw model.

Run on: October 6, 2004, 20:42:21 ; Search time 39 Seconds  
 (without alignments)  
 137.534 Million cell updates/sec

Title: US-09-982-259B-7  
 Perfect score: 89  
 Sequence: 1 GMTFRAQEAGAFLTGAAC 17

Scoring table: BL050462  
 Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : SPTREMBL 25:\*

1: sp\_archea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_invertebrate:\*

5: sp\_human:\*

6: sp\_invertebrate:\*

7: sp\_mammal:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rhod:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriip:\*

17: sp\_archeap:\*

Q9alm3 saccaropol  
 Q9yxr6 aeropyrum P  
 Q89863 clostridium  
 Q9pap5 ureaplasma  
 Q8rl1y mycoplasma  
 Q8rlx2 mycoplasma  
 Q8hco0 oryza sativ  
 Q98cq2 rhizobium 1  
 Q8kms3 salmonella  
 Q8kws0 borrelia bu  
 Q59701 schizosacch  
 Q9lkr3 nilotiana P  
 Q35727 mus musculus  
 Q80yc5 mus musculus  
 Q8kri6 ralstonia s  
 Q8zzh3 pyrobaculum  
 Q9hhu9 pseudomonas  
 Q9r610 escherichia  
 Q9zfs3 bacillus me  
 Q8at66 bacteroides  
 Q8kdl1 chlorobium  
 Q97160 clostridium  
 Q82q14 streptomyce  
 Q90sc1 meleagris g  
 Q815k5 gossypium h  
 Q9l1ws streptomyce  
 Q88ab8 pseudomonas  
 Q8dz36 streptococ

#### ALIGNMENTS

RESULT 1  
 O31361 ID O31361 PRELIMINARY; PRT; 243 AA.  
 AC O31361; 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DB Membrane protein A (Fragment).  
 GN BMPA.  
 OS Borrelia garinii.  
 OC Bacteria; Spirochaetes; Spirochaetales; Borrelia.  
 OX NCBI\_TAXID=9519;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=TN;  
 RX MEDLINE=98010210; PubMed=9350727;  
 RA Reissler D.; Hauser U.; Wilcke R.;  
 RT "Heterogeneity of BmpA (P39) among European Isolates of Borrelia burgdorferi Sensu Lato and Influence of Interspecies Variability on Serodiagnosis.";  
 RL J. Clin. Microbiol. 35:2752-2758 (1997).  
 DR GO:0008289; CA65882-1; -.  
 DR InterPro; IPR03760; Bmp.  
 DR Pf02608; Bmp; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 243 243  
 SQ SEQUENCE 243 AA; 26070 MW; 0E750B5E5BD0D6F8 CRC64;  
 DR GO:0008289; CA65882-1; -.  
 DR Local Similarity 100%; Pred. No. 0.00025;  
 DR保守性保守性 0; Mismatches 0; Indels 0; Gaps 0;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7.2	80.9	243	031361	031361 borrelia ga
2	7.2	80.9	264	031358	031359 borrelia ga
3	7.2	80.9	325	Q98776	Q9r776 borrelia bu
4	7.2	80.9	325	Q98777	Q9r777 borrelia bu
5	7.2	80.9	339	081960	Q87960 borrelia bu
6	7.2	80.9	339	2 Q9SSC1	Q9s6c1 borrelia bu
7	7.2	80.9	339	2 Q9FP92	Q9fd92 borrelia bu
8	6.9	77.5	264	2 O31361	031359 borrelia ga
9	4.5	50.6	374	16 Q8EL43	Q8el43 oceanobacil
10	4.5	50.6	500	12 Q9NF79	Q68979 human herpe
11	4.5	50.6	626	12 Q9QNF4	Q9qnf4 human herpe
12	4.5	50.6	626	12 Q9QNF5	Q9qnf5 human herpe
13	4.5	50.6	626	12 Q9NF78	Q68978 human herpe
14	4.5	50.6	626	12 Q9NF6	Q9qnf6 human herpe
15	4.4	49.4	355	16 Q81WP4	Q81wp4 bacillus an
16	4.4	49.4	361	16 Q81A05	Q81a05 bacillus ce

RESULT 2

RESULT 4  
 ID Q9R777 PRELIMINARY; PRT; 325 AA.  
 AC Q9R777; PRELIMINARY; PRT; 325 AA.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE Membrane protein A (Fragment).  
 GN BmpA.  
 OS *Borrelia garinii*; *Bacteria*; *Spirochaetes*; *Spirochaetales*; *Borrelia*.  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 STRAIN=px1;  
 MEDLINE=98010210; PubMed=9350727;  
 RA Roessler D.; Hauser U.; Wiliske B.;  
 RT "heterogeneity of BmpA (P39) among European Isolates of *Borrelia burgdorferi* Sensu Lato and Influence of Interspecies Variability on Serodiagnosis";  
 RT Serodiagnosis";  
 RL J. Clin. Microbiol. 35:2752-2758(1997).  
 DR EMBL: X97236; CAA65875.1;  
 GO: GO:0008289; F1lipid binding; IEA.  
 DR InterPro: IPR003760; Bmp.  
 PEAM; PF02608; Bmp; 1.  
 FT NON\_TER 1 1  
 FT NON\_TER 264 264  
 SQ SEQUENCE 264 AA; 28284 MW; 5493E14612E127D4 CRC64;  
 Query Match 80.9%; Score 72; DB 2; Length 325;  
 Best Local Similarity 100.0%; Pred. No. 0.00034;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GMTFRAQEGAFLTG 14  
 Db 115 GMTFRAQEGAFLTG 128

RESULT 5  
 ID Q9R760 PRELIMINARY; PRT; 339 AA.  
 AC Q9R760; PRELIMINARY; PRT; 339 AA.  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DE Membrane protein A (Fragment).  
 GN BmpA.  
 OS *Borrelia burgdorferi* (Lyme disease spirochete).  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 STRAIN=B31;  
 MEDLINE=98010210; PubMed=9350727;  
 RA Roessler D.; Hauser U.; Wiliske B.;  
 RT "heterogeneity of BmpA (P39) among European Isolates of *Borrelia burgdorferi* Sensu Lato and Influence of Interspecies Variability on Serodiagnosis";  
 RT Serodiagnosis";  
 RL J. Clin. Microbiol. 35:2752-2758(1997).  
 DR EMBL: X97235; CAA55874.1;  
 GO: GO:0008289; F1lipid binding; IEA.  
 DR InterPro: IPR003760; Bmp.  
 PEAM; PF02608; Bmp; 1.  
 SQ SEQUENCE 339 AA; 37024 MW; D64361DB0CA6C972 CRC64;  
 Query Match 80.9%; Score 72; DB 2; Length 339;  
 Best Local Similarity 100.0%; Pred. No. 0.00035;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GMTFRAQEGAFLTG 14  
 Db 115 GMTFRAQEGAFLTG 128

RESULT 3  
 ID Q9R776 PRELIMINARY; PRT; 325 AA.  
 AC Q9R776; PRELIMINARY; PRT; 325 AA.  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE Membrane protein A (Fragment).  
 GN BmpA.  
 OS *Borrelia burgdorferi* (Lyme disease spirochete).  
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 STRAIN=T255;  
 MEDLINE=98010210; PubMed=9350727;  
 RA Roessler D.; Hauser U.; Wiliske B.;  
 RT "heterogeneity of BmpA (P39) among European Isolates of *Borrelia burgdorferi* Sensu Lato and Influence of Interspecies Variability on Serodiagnosis";  
 RT Serodiagnosis";  
 RL J. Clin. Microbiol. 35:2752-2758(1997).  
 DR EMBL: X97240; CAA65879.1;  
 GO: GO:0008289; F1lipid binding; IEA.  
 DR InterPro: IPR003760; Bmp.  
 PEAM; PF02608; Bmp; 1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 325 AA; 35402 MW; 2F1D43E151CB0663 CRC64;  
 Query Match 80.9%; Score 72; DB 2; Length 325;  
 Best Local Similarity 100.0%; Pred. No. 0.00034;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GMTFRAQEGAFLTG 14  
 Db 115 GMTFRAQEGAFLTG 128

RESULT 6	Q9S6C1	PRELIMINARY;	PRT;	339 AA.	DT	01-JAN-1998 (TrEMBLrel. 05, Created)
	ID				DT	01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
	AC	Q9S6C1;			DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
	DT	01-MAY-2000 (TrEMBLrel. 13, Created)			DE	Membrane protein A (Fragment).
	DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			GN	BMPA.
	DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			OS	Borrelia garinii.
	DE	Immunodominant antigen P39.			OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
	OS	Borrelia burgdorferi (Lyme disease spirochete).			OX	NCBI_TaxID=29519;
	OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.			RN	[1]
	OX	NCBI_TaxID=139;			RP	SEQUENCE FROM N.A.
	RN	SEQUENCE FROM N.A.			RC	RA
	RC	STRAIN-BT01;			RT	Rossbauer D., Hauser U., Wilke B.
	RA	Tong Y.P., Feng F.B., Bi S.L., Zhou G.P.,			RT	"Heterogeneity of BMPA (P39), among European Isolates of Borrelia burgdorferi Sensu Lato and Influence of Interspecies Variability on Serodiagnosis";
	RT	"Molecular cloning and sequencing of P39 gene of a Borrelia burgdorferi strain isolated from China";			RT	RL J. Clin. Microbiol. 35:2752-2758(1997).
	RT	Submitted (DBC-1998) to the EMBL/GenBank/DBJ databases.			RL	X97742; CAA5881.1;
	EMBL	AF116774; AAD21046.1;			DR	DR GO; GO:0008289; F:lipid binding; IEA.
	DR	GO; GO:0008289; F:lipid binding; IEA.			DR	DR InterPro; IPR003760; Bmp.
	DR	InterPro; IPR003760; Bmp.			DR	DR Pfam; PF02608; Bmp; 1.
	DR	Pfam; PF02608; Bmp;			FT	FT NON_TER 264 1 1
	SQ	SEQUENCE 339 AA;	36969 MW;	A95ABA42EA79596D CRC64;	SQ	SEQUENCE 264 AA;
		Query Match 80.9%; Score 72; DB 2; Length 339;				28393 MW;
		Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;				CE0F18C91D0DA95D CRC64;
	Qy	1 GMTFRAQEGAFLTG 14			Qy	1 GMTFRAQEGAFLTG 14
	Db	129 GMTFRAQEGAFLTG 142			Db	115 GMTFRAQEGAFLTG 128
RESULT 7	Q9FD92	PRELIMINARY;	PRT;	339 AA.	RESULT 9	Q8E143
	ID	Q9FD92;				ID
	AC	Q9FD92;				Q8E143
	DT	01-MAR-2001 (TrEMBLrel. 16, Created)				AC
	DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)				OBEL43;
	DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				OBEL43; PRELIMINARY;
	DE	BmpA.				PRT;
	OS	Borrelia burgdorferi (Lyme disease spirochete).				374 AA.
	OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.				
	OX	NCBI_TaxID=139;				
	RN	SEQUENCE FROM N.A.				
	RC	STRAIN-N40;				
	RX	Medline=21065112; PubMed=11136458;				
	RA	Dobrikova B.Y., Bugrysheva J., Cabello P.C.;				
	RT	"Two independent transcriptional units control the complex and simultaneous expression of the bmp paralogous chromosomal gene family in Borrelia burgdorferi.";				
	RT	in Borrelia burgdorferi. Mol. Microbiol. 39:370-379 (2001).				
	RL	DR EMBL; AF288609; AA:GO0584.1; -				
	DR	GO:0008289; F:lipid binding; IEA.				
	DR	InterPro; IPR003760; Bmp.				
	DR	Pfam; PF02608; Bmp; 1.				
	SQ	SEQUENCE 339 AA;	37056 MW;	FA90B7F0D8228920 CRC64;		DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
		Query Match 80.9%; Score 72; DB 2; Length 339;				KW Complete proteome.
		Best Local Similarity 100.0%; Pred. No. 0.00035; Indels 0; Gaps 0;				SQ SEQUENCE 374 AA;
	Qy	1 GMTFRAQEGAFLTG 14				40224 MW;
	Db	129 GMTFRAQEGAFLTG 142				E8680244EEB48A48 CRC64;
RESULT 8	O31358	PRELIMINARY;	PRT;	264 AA.	Qy	1 GMTFRAQEGAFLTGAA 16
	ID	O31358			Db	156 GITSESHOOGFLYGVAA 171
	AC					

RESULT 10

Q68379 PRELIMINARY; PRT; 500 AA.

AC Q68379; Q9ONP4; Q9ONP5; PRT; 626 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)  
01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DB 1\_9kD ORF.

GN AB.

OS Human herpesvirus 1.

OC Alphaherpesvirinae; Simplexvirus.

NCBI\_TaxID=10298;

[1]

SEQUENCE OP 1-63 FROM N.A.

RP PubMed=6313961; PubMed=3005609;

RX Costa R.H., Draper K.G., Banks L., Powell K.L., Cohen G.,  
Bisenberg R., Wagner E.K.; "High-resolution characterization of herpes simplex virus type 1 transcripts encoding alkaline exonuclease and a 50,000-dalton protein tentatively identified as a capsid protein." J. Virol. 48:1591-603 (1983).

RN [2]

SEQUENCE FROM N.A.

RP PubMed=8614106; PubMed=3005609;

RX Draper K.G., Devi-Rao G., Costa R.H., Blair E.D., Thompson R.L., Wagner E.K.; "Characterization of the genes encoding herpes simplex virus type 1 and type 2 alkaline exonucleases and overlapping proteins." J. Virol. 57:1032-1036 (1986).

RL EMBL; K02022; AAA4772.1; -.

DR GO:0003677; F:DNA binding; IEA.

DR GO:0004527; F:exonuclease activity; IEA.

DR InterPro; IPR001616; Herpes alk exo.

DR Pfam; PF01771; Herpes alk exo; 1.

DR PRINTS; PR00924; ALXENNUCLASE.

SEQUENCE 500 AA; AE528A06E6FB361E CRC64;

Query Match Score 45; DB 12; Length 500;  
Best Local Similarity 56.2%; Pred. No. 28;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GMTPRAQEGAFLTGAA 16  
Db 411 GVTFLIEDGAGLGA 426

RESULT 11

Q9ONP4 PRELIMINARY; PRT; 626 AA.

AC Q9ONP4; Q9ONP5; PRT; 626 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)  
01-OCT-2003 (TREMBLrel. 13, Last sequence update)

DB Alkaline deoxyribonuclease.

GN UN12.

OS Human herpesvirus 1.

OC Alphaherpesvirinae; Simplexvirus.

NCBI\_TaxID=10298;

RN SEQUENCE FROM N.A.

RP PubMed=92286792; PubMed=10350747;

RX Chiba A., Suzutani T., Saito M., Koyano S., Azuma M.; "Analysis of nucleotide sequence variations in herpes simplex virus types 1 and 2, and varicella-zoster virus." Acta Virol. 42:401-407 (1998).

RL EMBL; AB009265; BAA8404.2; -.

DR GO:0003677; F:DNA binding; IEA.

DR GO:0004527; F:exonuclease activity; IEA.

DR InterPro; IPR001616; Herpes alk exo.

DR Pfam; PF01771; Herpes alk exo; 1.

DR PRINTS; PR00924; ALXENNUCLASE.

SEQUENCE 626 AA; 67492 MW; F5F92710E0A5A2 CRC64;

Query Match Score 45; DB 12; Length 626;  
Best Local Similarity 56.2%; Pred. No. 35;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GMTPRAQEGAFLTGAA 16  
Db 537 GVTFLIEDGAGLGA 552

RESULT 12

Q9ONP5 PRELIMINARY; PRT; 626 AA.

AC Q9ONP5; Q9ONP6; PRT; 626 AA.

DT 01-MAY-2000 (TREMBLrel. 13, Created)  
01-OCT-2003 (TREMBLrel. 13, Last sequence update)

DB Alkaline deoxyribonuclease.

GN UN12.

OS Human herpesvirus 1.

OC Alphaherpesvirinae; Simplexvirus.

NCBI\_TaxID=10298;

RN SEQUENCE FROM N.A.

RP PubMed=99246799; PubMed=10358747;

RX Chiba A., Suzutani T., Saito M., Koyano S., Azuma M.; "Analysis of nucleotide sequence variations in herpes simplex virus types 1 and 2, and varicella-zoster virus." Acta Virol. 42:401-407 (1998).

RL EMBL; AB009265; BAA8404.2; -.

DR GO:0003677; F:DNA binding; IEA.

DR GO:0004527; F:exonuclease activity; IEA.

DR InterPro; IPR001616; Herpes alk exo.

DR Pfam; PF01771; Herpes alk exo; 1.

DR PRINTS; PR00924; ALXENNUCLASE.

SEQUENCE 626 AA; 67492 MW; F5F92710E0A5A2 CRC64;

Query Match Score 45; DB 12; Length 626;  
Best Local Similarity 56.2%; Pred. No. 35;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GMTPRAQEGAFLTGAA 16  
Db 537 GVTFLIEDGAGLGA 552

RESULT 13

Q68978 PRELIMINARY; PRT; 626 AA.

AC Q68978; Q68979; PRT; 626 AA.

DT 01-NOV-1996 (TREMBLrel. 01, Created)  
01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DB Alkaline deoxyribonuclease.

GN UN12.

OS Human herpesvirus 1.

OC Alphaherpesvirinae; Simplexvirus.

NCBI\_TaxID=10298;

RN SEQUENCE OF 1-189 FROM N.A.

RP PubMed=84036396; PubMed=6313961;

RX Costa R.H., Draper K.G., Banks L., Powell K.L., Cohen G., Bisenberg R., Wagner E.K.; "High-resolution characterization of herpes simplex virus type 1 transcripts encoding alkaline exonuclease and a 50,000-dalton protein tentatively identified as a capsid protein." J. Virol. 48:591-603 (1983).

DR GO:0004527; F:exonuclease activity; IEA.

DR InterPro; IPR001616; Herpes alk exo.

DR Pfam; PF01771; Herpes alk exo; 1.

RN [2]

RP SEQUENCE FROM N.A. PubMed=3005609;  
 RX MEDLINE=80144016; PubMed=3005609;  
 RA Draper K.G., Devi-Kao G., Costa R.H., Blair E.D., Thompson R.L.,  
 RA Wagner E.K.;  
 RT "Characterization of the genes encoding herpes simplex virus type 1."  
 RL J. Virol. 57:1023-1036 (1986).  
 DR EMBL; KO0022; AAA45771; -;  
 GO; GO:0003677; F:DNA binding; IEA.  
 GO; GO:004527; F:exonuclease activity; IEA.  
 InterPro; IPR001616; Herpes alk exo.  
 Pfam; PF01771; Herpes alk exo; I.  
 DR PRINTS; PR00924; ALKEKNCLASB.  
 KW Exonuclease.  
 SEQUENCE 626 AA; 67469 MW; A651D03A29C70260 CRC64;

Query Match 50.6%; Score 45; DB 12; Length 626;  
 Best Local Similarity 56.2%; Pred. No. 35;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 537 GMTFRAQEGAFLGTGAA 16

Db 537 GVTFLLEDGAGALGAA 552

RESULT 14  
 Q9NPF6 PRELIMINARY; PRT; 626 AA.  
 AC Q9NPF6;  
 DT 01-MAY-2000 (TREMBLrel. 13; Created)  
 DT 01-MAY-2000 (TREMBLrel. 13; Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)  
 DE Alkaline deoxyribonuclease.  
 GN U112.  
 OS Human herpesvirus 1.  
 OC Viruses; DNA viruses; no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 NCBI\_TaxID=10298;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=VR-3;  
 RX MEDLINE=99286799; PubMed=10358747;  
 RA Chiba A., Suzutani T., Saito M., Koyano S., Azuma M.;  
 RT "Analysis of nucleotide sequence variations in herpes simplex virus types 1 and 2, and varicella-zoster virus.";  
 RL Acta Virol. 42:401-407 (1998).  
 DR EMBL; AB009264; BRA8403.; -;  
 GO; GO:003677; F:DNA binding; IEA.  
 DR PRINTS; PR001616; Herpes alk exo.  
 DR PRINTS; PR00924; ALKEKNCLASB.  
 SEQUENCE 626 AA; 67558 MW; 68148732098454E7 CRC64;

Query Match 50.6%; Score 45; DB 12; Length 626;  
 Best Local Similarity 56.2%; Pred. No. 35;  
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 GMTFRAQEGAFLGTGAA 16

Db 537 GVTFLLEDGAGALGAA 552

RESULT 15  
 Q81WP4 PRELIMINARY; PRT; 355 AA.  
 ID Q81WP4;  
 AC Q81WP4;  
 DT 01-JUN-2003 (TREMBLrel. 24; Created)  
 DT 01-JUN-2003 (TREMBLrel. 24; Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)  
 DE Lipoprotein, Bmp family.  
 GN BA3927.  
 OS Bacillus anthracis (strain Ames).

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus .  
 NCBI\_TaxID=19894;  
 OX [1]  
 RN RP  
 SEQUENCE FROM N.A.  
 RX MEDLINE=22608414; PubMed=12721629;  
 RA Read T.D.; Peterson S.N., Tournasse N., Baillie L.W., Paulsen I.T.,  
 Nelson K.B., Tettelein H., Fouts D.E., Eisen J.A., Gill S.R.,  
 Holtzapfel E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,  
 Kolonay J.P., Beaman R.J., Dobson R.J., Brinkac L.M., Gwinn M.,  
 DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,  
 Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,  
 Benton J.J., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,  
 Berry K.J., Pautz R.D., Wolf A.M., Watkins K.L., Nieman W.C.,  
 Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,  
 Thomason B., Friedlander A.M., Hanna P.C., Koistola A.-B.,  
 Fraser C.M.;  
 RA "The genome sequence of *Bacillus anthracis* Ames and comparison to  
 closely related bacteria.";  
 RL Nature 423:81-86 (2003).  
 DR AE017035; AA227658.1; -.  
 DR EMBL; AE017035; AA227658.1; -.  
 DR TIGR; BA9327; -.  
 DR GO; GO:0008289; F:lipid binding; IEA.  
 DR InterPro; IPR003760; Bmp.  
 DR InterPro; IPR000437; Prok\_lipoprot\_S.  
 DR Pfam; PF02608; Bmp.1.  
 DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
 KW Lipoprotein; Complete protein; 1.  
 SQ SEQUENCE 355 AA; 38373 MW; C6584A9DDE59BF17 CRC64;  
 Query Match 49.4%; Score 44; DB 16; Length 355;  
 Best Local Similarity 57.1%; Pred. No. 28;  
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 MTFRQEGAFLGTGA 15

Db 138 ITFKDHEGSGFLVGA 151

Search completed: October 6, 2004, 20:49:04  
 Job time : 43 secs

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OM protein - protein search, using SW model

Run on: October 6, 2004, 20:48:11 ; Search time 17 Seconds  
(without alignments)

Perfect score: 89

Sequence: 1 GMTFRAQEGLFTGAAAC 17

Title: US-09-982-259b-7

Scoring table: BL0SUM62

Gapext: 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0\*

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cn2\_6\_ptodata/2/iaa/5A\_COMB.pep:\*

2: /cn2\_6\_ptodata/2/iaa/5B\_COMB.pep:\*

3: /cn2\_6\_ptodata/2/iaa/5A\_COMB.pep:\*

4: /cn2\_6\_ptodata/2/iaa/5B\_COMB.pep:\*

5: /cn2\_6\_ptodata/2/iaa/5CTUS\_COMB.pep:\*

6: /cn2\_6\_ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	7.2	80.9	339	1	US-09-957A-4	Sequence 4, Appli
2	43.5	48.9	492	3	US-09-036-987A-5	Sequence 5, Appli
3	43.5	48.9	492	3	US-09-30-700-5	Sequence 5, Appli
4	43.5	48.9	492	4	US-09-603-207-5	Sequence 5, Appli
5	4.2	47.2	341	1	US-08-396-957A-5	Sequence 5, Appli
6	4.1	46.1	111	1	US-08-466-886-43	Sequence 43, Appli
7	4.1	46.1	111	1	US-08-469-617-43	Sequence 43, Appli
8	4.1	46.1	202	4	US-09-252-991A-33035	Sequence 33035, A
9	4.1	46.1	231	4	US-09-489-039A-10973	Sequence 10973, A
10	4.0	44.9	339	0	US-09-071-035-80	Sequence 80, Appli
11	4.0	44.9	361	4	US-09-071-035-78	Sequence 78, Appli
12	4.0	44.9	362	4	US-09-134-000C-6004	Sequence 6004, Ap
13	4.0	44.9	375	4	US-09-134-000C-6005	Sequence 6005, Ap
14	4.0	44.9	460	2	US-08-677-049-10	Sequence 10, Appli
15	4.0	44.9	556	4	US-09-252-991A-27601	Sequence 27601, A
16	39.5	44.4	1891	2	US-08-804-227C-12	Sequence 12, Appli
17	39.5	44.4	1891	2	US-08-804-198-6	Sequence 6, Appli
18	38.5	43.3	613	4	US-09-331-568A-25	Sequence 25, Appli
19	3.8	42.7	749	4	US-09-489-7979	Sequence 7979, Ap
20	37.5	42.1	136	2	US-08-997-080-145	Sequence 145, Appli
21	37.5	42.1	136	2	US-08-997-362-145	Sequence 145, Appli
22	37.5	42.1	136	2	US-09-095-855-145	Sequence 145, Appli
23	37.5	42.1	136	4	US-09-324-542-145	Sequence 145, Appli
24	37.5	42.1	136	4	US-09-205-426-145	Sequence 145, Appli
25	37.5	42.1	1482	4	US-09-410-551B-21	Sequence 17, Appli
26	37.5	42.1	1488	4	US-09-410-551B-17	Sequence 23, Appli
27	37.5	42.1	1503	4	US-09-410-551B-23	

RESULT 1  
US-09-957A-4  
; Sequence 4, Application US/08396957A  
; Patent No. 5780041  
; GENERAL INFORMATION:  
; APPLICANT: SIMPSON, WARREN; SCHNAN, TOM G.  
; TITLE OF INVENTION: ANTIGENIC PROTEINS AND  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNegan, L.L.P.  
; STREET: 345 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTY: USA  
; ZIP: 10154  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: FLOPPY DISK  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC DOS/TMS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/396,957A  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 08/020,245  
; FILING DATE: 19-FEB-1993  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 07/664,731  
; FILING DATE: 05-MAY-1991  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 07/487,716  
; FILING DATE: 05-MAY-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: DOROTHY R. AUTH  
; REGISTRATION NUMBER: 36,434  
; REFERENCE/DOCKET NUMBER: 2026-4-018US4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 758-4800  
; TELEFAX: (212) 751-6849  
; TELE: 421792  
; INFORMATION FOR SEQ ID NO: 4:  
; LENGTH: 339  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein

HYPOTHETICAL: NC

ORIGINAL SOURCE:

STRAIN: *Borrelia burgdorferi*

INDIVIDUAL ISOLATE:

DEVELOPMENTAL STAGE:

HAPlotype:

TISSUE TYPE:

CELL TYPE:

CELL LINE:

ORGANELLE:

FEATURE:

NAME/KEY: p39,

LOCATION:

IDENTIFICATION METHOD:

OTHER INFORMATION: P39' protein

OTHER INFORMATION: Sequence.

US-08-396-95A-4

Query Match 80.9%; Score 72; DB 1; length 339;

Best Local Similarity 100.0%; Pred. No. 3.3e-05;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GMTFRAQEGAFLTG 14

Db 129 GMTFRAQEGAFLTG 142

RESULT 2

US-09-036-987A-5

Sequence 5, Application US/09036987A

GENERAL INFORMATION:

APPLICANT: Baltz, Richard H.

APPLICANT: Broughton, Mary C.

APPLICANT: Crawford, Kathryn P.

APPLICANT: Madduri, Krishnamurthy

APPLICANT: Merlo, Donald J.

APPLICANT: Treadaway, Patti J.

APPLICANT: Turner, Jan R.

APPLICANT: Waldron, Clive

TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide

TITLE OF INVENTION: Production

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dow AgroSciences LLC Patent Department

STREET: 9330 Zionsville Road

CITY: Indianapolis

STATE: Indiana

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/036,987A

FILING DATE: 09-MAR-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stuart, Donald R

REGISTRATION NUMBER: 28,479

REFERENCE/DOCKET NUMBER: 50,608

TELEPHONE: (317)337-4816

TELEFAX: (317)337-4847

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 4928 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-036-987A-5

Query Match 48.9%; Score 43.5; DB 3; Length 4928;

Best Local Similarity 66.7%; Pred. No. 1.2e+02;

Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 GMTFRAQEGAFLTG 15

Db 3383 GSTY-VREGAFLTG 3396

RESULT 3

US-09-370-700-5

Sequence 5, Application US/09370700

GENERAL INFORMATION:

APPLICANT: Baltz, Richard H.

APPLICANT: Broughton, Mary C.

APPLICANT: Crawford, Kathryn P.

APPLICANT: Madduri, Krishnamurthy

APPLICANT: Treadaway, Patti J.

APPLICANT: Waldron, Clive

APPLICANT: Turner, Jan R.

APPLICANT: Waldron, Clive

TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide

CURRENT APPLICATION NUMBER: US/09/370,700

CURRENT FILING DATE: 1999-08-09

EARLIER APPLICATION NUMBER: US 09/36987

EARLIER FILING DATE: 1998-03-09

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 4928

TYPE: PRT

ORGANISM: Saccharopolyspora spinosa

US-09-370-700-5

Query Match 48.9%; Score 43.5; DB 3; Length 4928;

Best Local Similarity 66.7%; Pred. No. 1.2e+02;

Matches 10; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

Qy 1 GMTFRAQEGAFLTG 15

Db 3383 GSTY-VREGAFLTG 3396

RESULT 4

US-09-603-207-5

Sequence 5, Application US/09603207B

GENERAL INFORMATION:

APPLICANT: Baltz, Richard H.

APPLICANT: Broughton, Mary C.

APPLICANT: Crawford, Kathryn P.

APPLICANT: Madduri, Krishnamurthy

APPLICANT: Treadaway, Patti J.

APPLICANT: Waldron, Clive

APPLICANT: Turner, Jan R.

APPLICANT: Waldron, Clive

TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide

CURRENT APPLICATION NUMBER: US/09/603,207B

CURRENT FILING DATE: 2000-06-23

EARLIER APPLICATION NUMBER: US/09/370,700

EARLIER FILING DATE: 1998-03-09

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 4928

TYPE: PRT

ORGANISM: Saccharopolyspora spinosa

US-09-603-207-5

Query Match 48.9%; Score 43.5; DB 4; Length 4928;

Best Local Similarity 66.7%; Pred. No. 1.2e+02; Mismatches 2; Indels 1; Gaps 1;

OTHER INFORMATION: P39a protein sequence  
US-08-396-957A-5

Query Match 47.2%; Score 42; DB 1; Length 341;  
Best Local Similarity 53.8%; Pred. No. 10; Mismatches 3; Indels 0; Gaps 0;

7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 MTRRAQEGAFLTG 14  
Db 135 VVERVQEGAFLAG 147

RESULT 5  
US-08-396-957A-5  
; Sequence 5, Application US/08396957A  
; Patent No. 5780041  
; GENERAL INFORMATION:  
; APPLICANT: SIMPSON, WARREN; SCHWAN, TOM G.  
; TITLE OF INVENTION: ANTIGENIC PROTEINS AND  
; GENES ENCODING SAME OF BORRELLIA BURGDORFERI.  
; NUMBER OF SEQUENCES: 9

ADRESSEE: MORGAN & FINNEGAN, L.L.P.  
STREET: 345 PARK AVENUE  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10154  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/396, 957A  
FILING DATE: 01-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/020, 245  
FILING DATE: 19-PEB-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/664, 731  
FILING DATE: 05-MAY-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/487, 716  
FILING DATE: 05-MAY-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: DOROTHY R. AUTH  
REGISTRATION NUMBER: 36, 434  
REFERENCE/DOCKET NUMBER: 2226-4018USA4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421192 431  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 341  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ORIGINAL SOURCE: Borrelia burgdorferi  
ORGANISM: Borrelia burgdorferi  
STRAIN: Sh-2-82  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE:  
HAPLOTYPE:  
TISSUE TYPE:  
CELL TYPE:  
CELL LINE:  
ORGANELLE:  
FEATURE:  
NAME/KEY: P39a  
LOCATION:  
IDENTIFICATION METHOD:

RESULT 6  
US-08-466-886-43  
; Sequence 43, Application US/08466886  
; Patent No. 5776677  
; GENERAL INFORMATION:  
; APPLICANT: Tsuji, Lap-Chee  
; APPLICANT: Riordan, John R.  
; APPLICANT: Rommens, Johanna M.  
; APPLICANT: Kerem, Bat-Sheva  
; APPLICANT: Collins, Francis S.  
; APPLICANT: Tanuzzi, Michael C.  
; APPLICANT: Drumm, Mitchell L.  
; APPLICANT: Buckwald, Manuel  
TITLE OF INVENTION: Cystic Fibrosis Gene  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX  
STREET: 1100 New York Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466, 886  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldstein, Jorge A.  
REGISTRATION NUMBER: 29, 021  
REFERENCE/DOCKET NUMBER: 1329.0010006  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 111 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: peptide  
MOLECULE TYPE: peptide  
US-08-466-886-43

Query Match 46.1%; Score 41; DB 1; Length 111;  
Best Local Similarity 62.5%; Pred. No. 43;  
Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 GMTRRAQEG--AFLTG 14  
Db 11 GVTFFHQPGMNAFLTG 26

RESULT 7  
US-08-469-617-43  
; Sequence 43, Application US/08469617  
; Patent No. 6201107  
; GENERAL INFORMATION:

APPLICANT: Teui, Lap-Chee  
 APPLICANT: Riordan, Joan R.  
 APPLICANT: Rommens, Johanna M.  
 APPLICANT: Kerem, Bat-Sheva  
 APPLICANT: Collins, Francis S.  
 APPLICANT: Iannuzzi, Michael C.  
 APPLICANT: Drumm, Mitchell L.  
 APPLICANT: Buckwald, Manuel L.  
 TITLE OF INVENTION: Cystic Fibrosis Gene  
 NUMBER OF SEQUENCES: 43  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: STEENE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.3.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/469,617  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldstein, Jorge A.  
 REGISTRATION NUMBER: 29,021  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 111 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: Peptide  
 US-08-469-617-43

Query Match 46.1%; Score 41; DB 3; Length 111;  
 Best Local Similarity 62.5%; Pred. No. 43;  
 Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 GATPRAQBG--AFLTG 14  
 Db 11 GVTFHMQPGMAGFLTG 26

RESULT 8  
 US-09-252-991A-33035  
 / Sequence 33035, Application US/09252991A  
 / Patent No. 6551795  
 / GENERAL INFORMATION:  
 / APPLICANT: Marc J. Rubenstein et al.  
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 / FILE REFERENCE: 107116.136  
 / CURRENT APPLICATION NUMBER: US/09/252,991A  
 / PRIOR FILING DATE: 1999-02-18  
 / PRIOR APPLICATION NUMBER: US 60/074,788  
 / PRIOR FILING DATE: 1998-02-18  
 / PRIOR APPLICATION NUMBER: US 60/094,190  
 / NUMBER OF SEQ ID NOS: 33142  
 / SEQ ID NO: 33135  
 / LENGTH: 222  
 / TYPE: PRT  
 / ORGANISM: *Pseudomonas aeruginosa*  
 / US-09-252-991A-33035

Query Match 46.1%; Score 41; DB 4; Length 202;  
 Best Local Similarity 80.0%; Pred. No. 8.6;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 EGAFITGAAAC 17  
 Db 184 EGFFITGAAAC 193

RESULT 9  
 US-09-489-039A-10973  
 / Sequence 10973, Application US/09489039A  
 / Patent No. 6610336  
 / GENERAL INFORMATION:  
 / APPLICANT: Gary Breton et. al.  
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 / FILE REFERENCE:  
 / CURRENT FILING DATE: 2000-01-27  
 / PRIOR APPLICATION NUMBER: US/09/489,039A  
 / PRIOR FILING DATE: 1999-01-29  
 / NUMBER OF SEQ ID NOS: 14342  
 / SEQ ID NO: 10973  
 / LENGTH: 231  
 / TYPE: PRT  
 / ORGANISM: *Klebsiella pneumoniae*  
 / US-09-489-039A-10973

Query Match 46.1%; Score 41; DB 4; Length 231;  
 Best Local Similarity 62.5%; Pred. No. 10;  
 Matches 10; Conservative 1; Mismatches 3; Indels 2; Gaps 1;

Qy 1 GATPRAQBG--AFLTG 14  
 Db 29 GVTFHMQPGMAGFLTG 44

RESULT 10  
 US-09-071-015-80  
 / Sequence 80, Application US/090710135  
 / Patent No. 6448043  
 / GENERAL INFORMATION:  
 / APPLICANT: Gil H. Choi  
 / TITLE OF INVENTION: *Enterococcus faecalis* Polynucleotides and Polypeptides  
 / NUMBER OF SEQUENCES: 4,956  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Human Genome Sciences, Inc.  
 / STREET: 9410 Key West Avenue  
 / CITY: Rockville  
 / STATE: Maryland  
 / COUNTRY: USA  
 / ZIP: 20850  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Disquette 3.50 inch, 1.4Mb storage  
 / COMPUTER: HP Vectra 416/33  
 / OPERATING SYSTEM: MSDOS version 6.2  
 / SOFTWARE: ASCII Text  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/071,035  
 / FILING DATE:  
 / CLASSIFICATION:  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER:  
 / FILING DATE:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: A. Anders Brooks  
 / REGISTRATION NUMBER: 36,373  
 / PRIORITY/DOCKET NUMBER: PB36952  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (301) 309-8504  
 / TELEFAX: (301) 309-8512  
 / INFORMATION FOR SEQ ID NO: 80:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 339 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-071-035-80

Query Match 44.9%; Score 40; DB 4; Length 339;  
 Best Local Similarity 57.1%; Pred. No. 24;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 TFRQEGAFLTGAA 16  
 Db 126 TFRDNEAAYLAGVA 139

RESULT 11  
 US-09-071-035-78  
 ; Sequence 78, Application US/09071035  
 ; Patent No. 6448043

GENERAL INFORMATION:  
 APPLICANT: Gil H. Choi  
 TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
 NUMBER OF SEQUENCES: 496  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Human Genome Sciences, Inc.  
 STREET: 9410 Key West Avenue  
 CITY: Rockville  
 STATE: Maryland  
 COUNTY: USA  
 ZIP: 20850

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage  
 COMPUTER: HP Vectra 486/33  
 OPERATING SYSTEM: MS DOS version 6.2  
 SOFTWARE: ASCII Text  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/071,035  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: A. Anders Brookes  
 REGISTRATION NUMBER: 36 373  
 REFERENCE/DOCKET NUMBER: PB369P2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (301) 309-8504  
 INFORMATION FOR SEQ ID NO: 78:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 361 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-071-035-78

Query Match 44.9%; Score 40; DB 4; Length 361;  
 Best Local Similarity 57.1%; Pred. No. 26;  
 Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 QY 3 TFRQEGAFLTGAA 16  
 Db 148 TFRDNEAAYLAGVA 161

RESULT 12  
 US-09-134-000C-6004  
 ; Sequence 6004, Application US/09134000C  
 ; Patent No. 6617156

GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al.  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
 FILE REFERENCE: 032796-032  
 CURRENT APPLICATION NUMBER: US/09/134,000C  
 PRIORITY APPLICATION NUMBER: US-09-134-000C-6005  
 PRIORITY FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 6812  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 6004  
 LENGTH: 362  
 TYPE: PRT  
 ORGANISM: Enterococcus faecalis  
 US-09-134-000C-6004

RESULT 13  
 US-09-134-000C-6005  
 ; Sequence 6005, Application US/09134000C  
 ; Patent No. 6617156

GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al.  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
 FILE REFERENCE: 032796-032  
 CURRENT APPLICATION NUMBER: US/09/134,000C  
 PRIORITY APPLICATION NUMBER: US-09-134-000C-6005  
 PRIORITY FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 6812  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 6005  
 LENGTH: 375  
 TYPE: PRT  
 ORGANISM: Enterococcus faecalis  
 US-09-134-000C-6005

RESULT 14  
 US-09-134-000C-6005  
 ; Sequence 10, Application US/09134000C  
 ; Patent No. 6617156

GENERAL INFORMATION:  
 APPLICANT: Guimaraes, M. Jorge  
 APPLICANT: Bazan, J. Fernando  
 APPLICANT: McClanahan, Terrill K.  
 APPLICANT: Zlotnik, Albert  
 TITLE OF INVENTION: PURIFIED MAMMALIAN NUCLEIC ACIDS; ANTIBODIES;  
 NUMBER OF SEQUENCES: 12

GENERAL INFORMATION:  
 ADDRESS: DNAX Research Institute  
 STREET: 901 California Avenue  
 CITY: Palo Alto  
 STATE: California

RESULT 15  
 US-09-134-000C-6004  
 ; Sequence 6004, Application US/09134000C  
 ; Patent No. 6617156

COUNTRY: USA  
 ZIP: 94304-1104  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/677,049  
 FILING DATE: 03-JUL-1996  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 60/000,788  
 FILING DATE: 03-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ching, Edwin P.  
 REGISTRATION NUMBER: 34,090  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-852-3196  
 TELEFAX: 415-496-1200  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 460 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 117..149  
 OTHER INFORMATION: /note= "Encompasses TM 4 of Figure  
 OTHER INFORMATION: 4"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 328..362  
 OTHER INFORMATION: /note= "Encompasses TM 9 of Figure  
 OTHER INFORMATION: 4"  
 FEATURE:  
 NAME/KEY: Region  
 LOCATION: 365..392  
 OTHER INFORMATION: /note= "Encompasses TM 10 of Figure  
 OTHER INFORMATION: 4"  
 SEQ ID NO: 677-049-10  
 Query Match 44.9%; Score 40; DB 2; Length 460;  
 Best Local Similarity 47.1%; Pred. No. 34;  
 Matches 8; Conservative 1; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 GMTFRAQEGAFITGAA 16  
 QY 288 GGTFRCPGSSVSTA 303  
 Search completed: October 6, 2004, 20:56:48  
 Job time : 19 secs

ORGANISM: *Pseudomonas aeruginosa*  
 US-09-252-991A-27601  
 Query Match 44.9%; Score 40; DB 4; Length 556;  
 Best Local Similarity 50.0%; Pred. No. 43;  
 Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 GMTFRAQEGAFITGAA 16  
 QY 288 GGTFRCPGSSVSTA 303

RESULT 15  
 S-09-252-991A-27601  
 Sequence 27601, Application US/09252991A  
 Patent No. 6551795  
 GENERAL INFORMATION:  
 APPLICANT: Marc J. Rubenstein et al.  
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*  
 TITLE OF INVENTION: *AERUGINOSA* FOR DIAGNOSTICS AND THERAPEUTICS  
 CURRENT APPLICATION NUMBER: US/09/252,991A  
 FILE REFERENCE: 107196..136  
 CURRENT FILING DATE: 1999-02-18  
 PRIOR APPLICATION NUMBER: US 60/074,788  
 PRIOR FILING DATE: 1998-02-18  
 PRIOR APPLICATION NUMBER: US 60/094,190  
 PRIOR FILING DATE: 1998-07-27  
 NUMBER OF SEQ ID NOS: 33142  
 SEQ ID NO: 27601  
 LENGTH: 556  
 TYPE: PPT

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OM protein - protein search, using SW model

Run on: October 6, 2004, 20:49:12 ; Search time 128 Seconds  
(without alignments) ; 42.739 Million cell updates/sec

Title: US-09-982-259B-7  
Scoring table: BLOSUM62  
Perfect score: 89  
Sequence: 1 GMMTPRAOEGAFLGAC 17

Scoring table: BLOSUM62  
Gapext 0.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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3: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us06\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us05\_PUBCOMB.pep:\*

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6: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us08\_PUBCOMB.pep:\*

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9: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us09\_PUBCOMB.pep:\*

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11: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us09\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us10\_PUBCOMB.pep:\*

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16: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us10c\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpa/ptcpaa/us60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB ID	Description
1	72	80.9	14	9 US-09-982-264-7	Sequence 7, Appli
2	72	80.9	14	9 US-09-982-259-7	Sequence 7, Appli
3	72	80.9	14	10 US-09-982-255-7	Sequence 7, Appli
4	72	80.9	14	10 US-09-982-287-7	Sequence 7, Appli
5	4.6	51.7	1218	16 US-10-337-963-128680	Sequence 2, Appli
6	4.5	50.6	626	16 US-10-656-888-2	Sequence 5, Appli
7	43.5	48.9	4928	16 US-10-329-148A-5	Sequence 147037, Appli
8	4.2	47.2	1811	16 US-10-437-963-147037	Sequence 231687, Appli
9	4.1	46.1	102	12 US-10-424-593-231687	Sequence 9, Appli
10	4.1	46.1	247	9 US-09-419-040-9	Sequence 8098, Appli
11	4.1	46.1	375	14 US-10-156-751-8088	Sequence 5, Appli
12	4.1	46.1	1366	16 US-10-203-255-5	Sequence 239471, Appli
13	4.0	44.9	99	12 US-10-424-599-239471	Sequence 22373, Appli
14	4.0	44.9	117	15 US-10-194-249-2373	Sequence 220111, Appli
15	4.0	44.9	188	12 US-10-424-599-220111	Sequence 150848, Appli

RESULT 1 ; Sequence 7, Application US/09982264

Patent No. US2002106706A1

GENERAL INFORMATION:

APPLICANT: Qiu, Bo

APPLICANT: Stein, Stanley

APPLICANT: Brunner, Michael

APPLICANT: Katz, Michael

APPLICANT: Zhang, Guobiao

APPLICANT: Sigal, Leonard

TITLE OF INVENTION: Immunological Test Kit with *Borellia burgdorferi* Epitope

FILE REFERENCE: 271/288

CURRENT APPLICATION NUMBER: US/09/982,264

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 7

LENGTH: 14

TYPE: PRT

ORGANISM: *Borellia burgdorferi*

US-09-982-264-7

Query	Match	Similarity	Score	DB	Length
Qy	1	GMTFRAQEGAFLTG	14		
Db	1	GMTFRAQEGAFLTG	14		
Qy	1	GMTFRAQEGAFLTG	14		
Db	1	GMTFRAQEGAFLTG	14		

RESULT 2 ; Sequence 7, Application US/09982259

Publication No. US2002197271A1

GENERAL INFORMATION:

APPLICANT: Qiu, Bo

APPLICANT: Stein, Stanley  
 APPLICANT: Brunner, Michael  
 APPLICANT: Katz, Michael  
 APPLICANT: Zhang, Guobao  
 APPLICANT: Sigal, Leonard  
 TITLE OF INVENTION: *Borellia burgdorferi* Epitope Peptides  
 FILE REFERENCE: 271/289  
 CURRENT APPLICATION NUMBER: US/09/982,259  
 CURRENT FILING DATE: 2001-10-17  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 7  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: *Borellia burgdorferi*  
 US-09-982-259-7

Query Match 80.9%; Score 72; DB 9; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GMTFRAQEGAFLTG 14  
 Db 1 GMTFRAQEGAFLTG 14

RESULT 3  
 Sequence 7, Application US/09982265  
 Publication No. US20030040126A1  
 GENERAL INFORMATION:  
 APPLICANT: Qiu, Bo  
 APPLICANT: Stein, Stanley  
 APPLICANT: Brunner, Michael  
 APPLICANT: Katz, Michael  
 APPLICANT: Zhang, Guobao  
 APPLICANT: Sigal, Leonard  
 TITLE OF INVENTION: Immunological Test Kit with Immunologically Invisible Carrier  
 FILE REFERENCE: 271/287  
 CURRENT APPLICATION NUMBER: US/09/982,265  
 CURRENT FILING DATE: 2001-10-17  
 NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 7  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: *Borellia burgdorferi*  
 US-09-982-265-7

Query Match 80.9%; Score 72; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GMTFRAQEGAFLTG 14  
 Db 1 GMTFRAQEGAFLTG 14

RESULT 4  
 Sequence 7, Application US/09982287  
 Publication No. US20030040127A1  
 GENERAL INFORMATION:  
 APPLICANT: Qiu, Bo  
 APPLICANT: Stein, Stanley  
 APPLICANT: Brunner, Michael  
 APPLICANT: Katz, Michael  
 APPLICANT: Zhang, Guobao  
 APPLICANT: Sigal, Leonard  
 TITLE OF INVENTION: Multiple Epitopes Connected by Carrier  
 FILE REFERENCE: 271/900  
 CURRENT APPLICATION NUMBER: US/09/982,287  
 CURRENT FILING DATE: 2001-10-17

NUMBER OF SEQ ID NOS: 7  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 7  
 LENGTH: 14  
 TYPE: PRT  
 ORGANISM: *Borellia burgdorferi*  
 US-09-982-287-7

Query Match 80.9%; Score 72; DB 10; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GMTFRAQEGAFLTG 14  
 Db 1 GMTFRAQEGAFLTG 14

RESULT 5  
 Sequence 128830, Application US/10437963  
 Publication No. US2004012343A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa, Thomas J.  
 APPLICANT: Kovacic, David K.  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 APPLICANT: Wu, Wei  
 APPLICANT: Boutharou, Andrey A.  
 APPLICANT: Barazuk, Brad  
 APPLICANT: Li, Ping  
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 Plants and Uses Thereof for Plant Improvement  
 FILE REFERENCE: 38-21(53221)B  
 CURRENT APPLICATION NUMBER: US/10/437,963  
 CURRENT FILING DATE: 2003-05-14  
 NUMBER OF SEQ ID NOS: 204956  
 SEQ ID NO: 128860  
 LENGTH: 1218  
 TYPE: PRT  
 ORGANISM: *Oryza sativa*  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT4530\_31010C.1.pep  
 US-10-437-963-128860

Query Match 51.7%; Score 46; DB 16; Length 1218;  
 Best Local Similarity 61.5%; Pred. No. 58;  
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MTTFRAQEGAFLTG 14  
 Db 11166 VTPPAKKGFLAG 1178

RESULT 6  
 Sequence 2, Application US/10656868  
 Publication No. US20040141994A1  
 GENERAL INFORMATION:  
 APPLICANT: University of Connecticut  
 APPLICANT: Weiller, Sandra K  
 APPLICANT: Bacher, Reuven, Nina  
 APPLICANT: Myers, Richard S  
 TITLE OF INVENTION: Viral Recombinases, Related Articles and Methods of Use Thereof  
 FILE REFERENCE: UCT-0039  
 CURRENT APPLICATION NUMBER: US/10/656,868  
 CURRENT FILING DATE: 2003-09-04  
 PRIOR APPLICATION NUMBER: US 60/408,092  
 PRIOR FILING DATE: 2002-09-04  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 2  
 LENGTH: 626  
 TYPE: PRT

ORGANISM: Herpes simplex virus 1  
 PUBLICATION INFORMATION:  
 DATABASE ACCESION NUMBER: GI 119693  
 DATABASE ENTRY DATE: 1992-05-01  
 RELEVANT RESIDUES: (1) .. (626) .. 01  
 US-10-656-868-2

Query Match 50.6%; Score 45; DB 16; Length 626;  
 Best Local Similarity 56.2%; Pred. No. 42; Mismatches 4; Indels 0; Gaps 0;  
 Matches 9; Conservative 3; Gaps 0;

Qy 1 GATTCRAGCAGTGTGAA 16  
 Db 537 GTTFRLSGAGAGLGR 552

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RESULT 7  
 US-10-329-148A-5  
 Sequence 5, Application US/10329148A  
 PUBLICATION NO. US20040023343A1.  
 GENERAL INFORMATION:  
 APPLICANT: Baltz, Richard H.  
 APPLICANT: Broughton, Mary C.  
 APPLICANT: Crawford, Kathryn P.  
 APPLICANT: Madduri, Krishnamurthy  
 APPLICANT: Treadway, Patti J.  
 APPLICANT: Turner, Jan R.  
 APPLICANT: Waldron, Clive  
 FILE REFERENCE: 50489 DIV1  
 CURRENT APPLICATION NUMBER: US/10/329,148A  
 CURRENT FILING DATE: 2002-12-23  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/03/603,207B  
 PRIOR FILING DATE: EARLIER FILING DATE: 2000-06-23  
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/370,700  
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-03-09  
 NUMBER OF SEQ ID NOS: 39  
 SOFTWARE: Patentin Ver. 2.0  
 SEQ ID NO 5  
 LENGTH: 4928  
 TIPS: PRT  
 ORGANISM: Saccharoplyspora spinosa  
 US-10-329-148A-5

Query Match 48.9%; Score 43.5; DB 16; Length 4928;  
 Best Local Similarity 66.7%; Pred. No. 7.2e+02; Mismatches 2; Indels 1; Gaps 1;  
 Matches 10; Conservative 2; Gaps 1;

Qy 1 GATTCRAGCAGTGTGAA 15  
 Db 3383 GATY-VREGAFLGAA 3396

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RESULT 8  
 US-10-437-963-147037  
 Sequence 147037, Application US/10437963  
 PUBLICATION NO. US004023341A1.  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa, Thomas J.  
 APPLICANT: Kovalic, David K.  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 APPLICANT: Wu, Wei  
 APPLICANT: Boukharov, Andrey A.  
 APPLICANT: Barbatuk, Brad  
 APPLICANT: Li, Fang  
 TITLE OF INVENTION: Plants and Other Molecules Associated With  
 FILE REFERENCE: 38-21(53221)B  
 CURRENT FILING DATE: 2003-05-14  
 NUMBER OF SEQ ID NOS: 204966  
 SEQ ID NO 147037

Query Match 48.1%; Score 41; DB 9; Length 247;  
 Best Local Similarity 42.9%; Pred. No. 75;

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RESULT 9  
 US-10-424-599-231687  
 Sequence 231687, Application US/10424599  
 PUBLICATION NO. US20040031072A1.  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa, Thomas J.  
 APPLICANT: Kovalic, David K.  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 FILE REFERENCE: 38-21(53223)B  
 CURRENT APPLICATION NUMBER: US/10/424,599  
 NUMBER OF SEQ ID NOS: 285684  
 SEQ ID NO 231687  
 LENGTH: 102  
 TIPS: PRT  
 ORGANISM: Glycine max  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT3847\_51236C.1.pep  
 US-10-424-599-231687

Query Match 46.1%; Score 41; DB 12; Length 102;  
 Best Local Similarity 50.0%; Pred. No. 29; Mismatches 8; Indels 0; Gaps 0;

Qy 2 MTTRAGCAGAFLTGAC 17  
 Db 52 MTMALPREGAFLAGLIC 67

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RESULT 10  
 US-09-479-040-9  
 Sequence 9, Application US/09479040  
 PUBLICATION NO. US20020182690A1.  
 GENERAL INFORMATION:  
 APPLICANT: McCoil, Gabriel J.  
 APPLICANT: Cannon, Maura C.  
 APPLICANT: Cannon, Francis C.  
 APPLICANT: Valentini, Henry E.  
 APPLICANT: Grays, Kenneth J.  
 TITLE OF INVENTION: POLYHYDROXYALKANOATE BIOSYNTHESIS ASSOCIATED PROTEINS  
 FILE REFERENCE: NOBT212  
 CURRENT APPLICATION NUMBER: US/09/479,040  
 NUMBER OF SEQ ID NOS: 29  
 SEQ ID NO 9  
 LENGTH: 247  
 TIPS: PRT  
 ORGANISM: Bacillus megaterium  
 US-09-479-040-9

Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0; LENGTH: 1366  
 Qy 1 GMTERAQOBGAFLTG 24  
 Db 223 GVVYLARDGAYTG 236

RESULT 11  
 US-10-156-761-8098  
 Sequence 8098, Application US/10156761  
 Publication No. US20040119018A1  
 GENERAL INFORMATION:  
 APPLICANT: OMURA, SATOSHI  
 APPLICANT: IKEDA, HARUO  
 APPLICANT: ISHIKAWA, JUN  
 APPLICANT: HORIKAWA, HIROSHI  
 APPLICANT: SHIDA, TADAYOSHI  
 APPLICANT: SAKAKI, YOSHITAKI  
 APPLICANT: HATTORI, MASAHIRO  
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 FILE REFERENCE: 249-262  
 CURRENT APPLICATION NUMBER: US/10/156,761  
 CURRENT FILING DATE: 2002-05-29  
 PRIORITY NUMBER: JP 2001-204099  
 PRIORITY NUMBER: JP 2001-204099  
 PRIORITY NUMBER: JP 2001-272697  
 PRIORITY NUMBER: JP 2001-272697  
 PRIORITY NUMBER: JP 2001-08-02  
 SEQ ID NO: 8098  
 LENGTH: 375  
 TYPE: PRT  
 ORGANISM: Streptomyces avermitilis  
 US-10-156-761-8098

Query Match Score 41; DB 16; Length 1366;  
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 TYPE: PRT  
 ORGANISM: Streptomyces noursei ATCC 11455  
 US-10-203-295-5

Query Match Score 41; DB 16; Length 1366;  
 Best Local Similarity 80.0%; Pred. No. 4.8e+02;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 TYPE: PRT  
 ORGANISM: Streptomyces noursei ATCC 11455  
 US-10-203-295-5

RESULT 13  
 US-10-424-599-239471  
 Sequence 239471, Application US/10424599  
 Publication No. US20040031072A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa, Thomas J  
 APPLICANT: Kovacic, David K  
 APPLICANT: Zhou, Yihua  
 APPLICANT: Cao, Yongwei  
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 FILE REFERENCE: 38-21(53223)B  
 CURRENT APPLICATION NUMBER: US/10/424,599  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 285684  
 SEQ ID NO: 239471  
 LENGTH: 99  
 TYPE: PRT  
 ORGANISM: Glycine max  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT3847\_58268C.1.pep  
 US-10-424-599-239471

Query Match Score 40; DB 12; Length 99;  
 Best Local Similarity 66.7%; Pred. No. 4.1e+02;  
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 TYPE: PRT  
 ORGANISM: Glycine max  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT3847\_58268C.1.pep  
 US-10-424-599-239471

RESULT 14  
 US-10-194-749-2373  
 Sequence 2373, Application US/10094749  
 Publication No. US20030219741A1  
 GENERAL INFORMATION:  
 APPLICANT: ISOGAI, TAKAO  
 APPLICANT: SUGIYAMA, TOMOYASU  
 APPLICANT: WAKAMATSU, AI  
 APPLICANT: SATO, HIROTOKI  
 APPLICANT: ISHII, SHIZUKO  
 APPLICANT: YAMAMOTO, JUN-ICHI  
 APPLICANT: ISONO, YUUKO  
 APPLICANT: HIO, YURI  
 APPLICANT: OTSUKA, KAORU  
 APPLICANT: NAGAI, KEIICHI  
 APPLICANT: IRIE, RYOTARO  
 APPLICANT: TAMBCHIKA, ICHIRO  
 APPLICANT: SEKI, NAOHIKO  
 APPLICANT: YOSHIKAWA, TSUTOMO  
 APPLICANT: OTSUKA, MOTOUICHI  
 APPLICANT: NAGAHARI, KENJI  
 APPLICANT: MASURO, YASUHIKO  
 TITLE OF INVENTION: Novel genes encoding a nystatin polyketide synthase and their  
 FILE REFERENCE: 1181-265  
 CURRENT APPLICATION NUMBER: US/10/203,295  
 CURRENT FILING DATE: 2003-05-19  
 PRIOR APPLICATION NUMBER: PCT/GB 01/00509  
 PRIOR FILING DATE: 2001-02-08  
 PRIOR APPLICATION NUMBER: GB 0002840.7  
 PRIOR FILING DATE: 2000-02-08  
 PRIOR APPLICATION NUMBER: GB 0008786.6  
 PRIOR FILING DATE: 2000-04-10  
 PRIOR APPLICATION NUMBER: GB 0009387.2  
 PRIOR FILING DATE: 2000-04-14  
 NUMBER OF SEQ ID NOS: 49  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 5

RESULT 15  
 US-10-203-295-5  
 Sequence 295, Application US/10094749  
 Publication No. US20030219741A1  
 GENERAL INFORMATION:  
 APPLICANT: Zotchey, Sergey Borisovich  
 APPLICANT: Sekurova, Olga Nikalayivna  
 APPLICANT: Fjaervik, Epsen  
 APPLICANT: Braatzaa, Trine Brigitte  
 APPLICANT: Strom, Arne Reidar  
 APPLICANT: Valla, Svein  
 APPLICANT: Billingsen, Trond Erling  
 APPLICANT: Sietsa, Havard  
 APPLICANT: Gulliksen, Ole-Martin  
 TITLE OF INVENTION: Novel genes encoding a nystatin polyketide synthase and their  
 FILE REFERENCE: 1181-265  
 CURRENT APPLICATION NUMBER: US/10/203,295  
 CURRENT FILING DATE: 2003-05-19  
 PRIOR APPLICATION NUMBER: PCT/GB 01/00509  
 PRIOR FILING DATE: 2001-02-08  
 PRIOR APPLICATION NUMBER: GB 0002840.7  
 PRIOR FILING DATE: 2000-02-08  
 PRIOR APPLICATION NUMBER: GB 0008786.6  
 PRIOR FILING DATE: 2000-04-10  
 PRIOR APPLICATION NUMBER: GB 0009387.2  
 PRIOR FILING DATE: 2000-04-14  
 NUMBER OF SEQ ID NOS: 49  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 5

RESULT 16  
 US-10-203-295-5  
 Sequence 295, Application US/10094749  
 Publication No. US20030219741A1  
 GENERAL INFORMATION:  
 APPLICANT: Zotchey, Sergey Borisovich  
 APPLICANT: Sekurova, Olga Nikalayivna  
 APPLICANT: Fjaervik, Epsen  
 APPLICANT: Braatzaa, Trine Brigitte  
 APPLICANT: Strom, Arne Reidar  
 APPLICANT: Valla, Svein  
 APPLICANT: Billingsen, Trond Erling  
 APPLICANT: Sietsa, Havard  
 APPLICANT: Gulliksen, Ole-Martin  
 TITLE OF INVENTION: Novel genes encoding a nystatin polyketide synthase and their  
 FILE REFERENCE: 1181-265  
 CURRENT APPLICATION NUMBER: US/10/203,295  
 CURRENT FILING DATE: 2003-05-19  
 PRIOR APPLICATION NUMBER: PCT/GB 01/00509  
 PRIOR FILING DATE: 2001-02-08  
 PRIOR APPLICATION NUMBER: GB 0002840.7  
 PRIOR FILING DATE: 2000-02-08  
 PRIOR APPLICATION NUMBER: GB 0008786.6  
 PRIOR FILING DATE: 2000-04-10  
 PRIOR APPLICATION NUMBER: GB 0009387.2  
 PRIOR FILING DATE: 2000-04-14  
 NUMBER OF SEQ ID NOS: 49  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO 5

PRIOR APPLICATION NUMBER: 60/350,435  
 PRIOR FILING DATE: 2002-01-24  
 PRIOR APPLICATION NUMBER: JP 2001-328381  
 PRIOR FILING DATE: 2001-09-14  
 NUMBER OF SEQ ID NOS: 3391  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO: 2373  
 LENGTH: 117  
 TYPE: PRT

ORGANISM: Homo sapiens  
 US-10-094-749-2373

Query Match 44.9%; Score 40; DB 15; Length 117;  
 Best Local Similarity 40.0%; Pred. No. 50;  
 Matches 10; Conservative 1; Mismatches 6; Indels 8; Gaps 1;  
 Qy 1 GATTCATGGG-----ATPLTGAAAC 17  
 Db 21 GATLRLRTGGATGATGATGATGATGATGATGACC 45

RESULT 15  
 US-10-424-599-220111  
 Sequence 220111, Application US/10424599  
 Publication No. US2004031072A1  
 GENERAL INFORMATION:  
 APPLICANT: La Rosa Thomas J  
 APPLICANT: Kovalic David K  
 APPLICANT: Zhou Yihua  
 APPLICANT: Cao Yongwei  
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 FILE REFERENCE: 38-21(51223)B  
 CURRENT APPLICATION NUMBER: US/10424599  
 CURRENT FILING DATE: 2003-04-28  
 NUMBER OF SEQ ID NOS: 285684  
 SEQ ID NO: 220111  
 LENGTH: 188  
 TYPE: PRT  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT3847\_4078C.1.pep

ORGANISM: Glycine max  
 FEATURE:  
 OTHER INFORMATION: Clone ID: PAT\_MRT3847\_4078C.1.pep

Query Match 44.9%; Score 40; DB 12; Length 188;  
 Best Local Similarity 47.1%; Pred. No. 83;  
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
 Qy 1 GATTCATGGG-----ATPLTGAAAC 17  
 Db 31 GATLRLRTGGATGATGATGATGATGATGATGACC 47

Search completed: October 6, 2004, 21:00:21  
 Job time : 131 secs